

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 19, 2004, 13:30:29 ; Search time 53 Seconds  
(without alignments)

836.980 Million cell updates/sec

Title: US-09-716-356A-6

Perfect score: 812

Sequence: 1 YFGKLEKSLVIRNLNDQVL.....LKKEDELGDRSIMFTVQNED 157

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*

1: Genesep1980s:\*

2: Genesep1990s:\*

3: Genesep2000s:\*

4: Genesep2001s:\*

5: Genesep2002s:\*

6: Genesep2003as:\*

7: Genesep2003bs:\*

8: Genesep2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	811	99.9	157	2	AAW77077	Human int
2	811	99.9	157	3	AAV57570	Human int
3	811	99.9	157	4	AAV57570	Human int
4	811	98.9	157	4	AAV57570	Human int
5	811	99.9	157	4	AAV57570	Human int
6	811	99.9	157	5	AAV57570	Human int
7	811	99.9	157	5	AAV57570	Human int
8	811	99.9	157	5	AAV57570	Human int
9	811	99.9	157	6	AAV57570	Human int
10	811	99.9	157	6	AAV57570	Human int
11	811	99.9	157	6	AAV57570	Human int
12	811	99.9	157	6	AAV57570	Human int
13	811	99.9	157	7	AAV57570	Human int
14	811	99.9	158	3	AAV57570	Human int
15	811	99.9	177	6	AAV57570	Human int
16	811	99.9	180	2	AAV57570	Human int
17	811	99.9	193	2	AAV57570	Human int
18	811	99.9	193	2	AAV57570	Human int
19	811	99.9	193	4	AAV57570	Human int
20	811	99.9	193	4	AAV57570	Human int
21	811	99.9	193	5	AAV57570	Human int
22	811	99.9	233	5	AAV57570	Human int
23	811	99.9	536	5	AAV57570	Human int
24	811	99.9	588	5	AAV57570	Human int
25	811	99.9	1048	5	AAV57570	Human int

26	810	99.8	157	2	AAV57570	Human int
27	810	99.8	157	2	AAV57570	Human int
28	810	99.8	157	2	AAV57570	Human int
29	810	99.8	157	2	AAV57570	Human int
30	810	99.8	157	2	AAV57570	Human int
31	810	99.8	157	2	AAV57570	Human int
32	810	99.8	157	2	AAV57570	Human int
33	810	99.8	157	2	AAV57570	Human int
34	810	99.8	157	2	AAV57570	Human int
35	810	99.8	157	2	AAV57570	Human int
36	810	99.8	157	2	AAV57570	Human int
37	810	99.8	157	2	AAV57570	Human int
38	810	99.8	157	2	AAV57570	Human int
39	810	99.8	157	2	AAV57570	Human int
40	810	99.8	157	2	AAV57570	Human int
41	810	99.8	157	2	AAV57570	Human int
42	810	99.8	157	2	AAV57570	Human int
43	810	99.8	157	2	AAV57570	Human int
44	810	99.8	157	2	AAV57570	Human int
45	810	99.8	157	2	AAV57570	Human int

ALIGNMENTS

RESULT 1  
AAW77077  
ID AAW77077 standard; peptide; 157 AA.  
AC AAW77077;  
XX  
XX  
DT 16-NOV-1998 (first entry)  
XX  
DE Human interleukin 18.  
XX  
KW Human; interleukin-18; IL-18; osteoclast; hypercalcaemia; osteopenia;  
osteoclastoma Behcet's syndrome; osteosarcoma; arthropathy; osteoporosis;  
chronic rheumatoid arthritis; deformity ostitis; primary hyperthyroidism.  
XX  
OS Homo sapiens.  
XX  
PN EP861663-A2.  
XX  
PD 02-SEP-1998.  
XX  
PF 24-FEB-1998; 98EP-00301352.  
XX  
PR 25-FEB-1997; 97JP-00055468.  
XX  
XX (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.  
XX  
XX Gillespie MT, Horwood NJ, Udagawa N, Kurimoto M;  
XX  
XX WPI; 1998-448964/39.  
XX  
XX N-PSDB; AAV48226.  
XX  
XX Use of interleukin-18 to inhibit osteoclast formation - in treatment of  
e.g. hypercalcaemia, osteoclastoma, Behcet's syndrome, osteosarcoma,  
chronic rheumatoid arthritis, deformity ostitis, primary hyperthyroidism  
and osteoporosis.  
XX  
XX Claim 4; Page 18; 56pp; English.  
XX  
XX Interleukin-18 (IL-18) or a functional equivalent can be used for  
inhibition of osteoclast formation. IL-18 is used for treating or  
preventing osteoclast-related diseases e.g. hypercalcaemia, osteoclastoma  
Behcet's syndrome, osteosarcoma, arthropathy, chronic rheumatoid  
arthritis, deformity ostitis, primary hyperthyroidism, osteopenia and  
osteoporosis  
XX  
XX SQ Sequence 157 AA;  
XX  
XX Query Match 99.9%; Score 811; DB 2; Length 157;

Best Local Similarity 99.4%; Pred. No. 9.8e-83;  
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQNRPLFEDMTSDCRDNAPRTIFIISMYSKDSQPRGM 60  
DB 1 YFGKLESKLSVIRNLNDQVLFIDQNRPLFEDMTSDCRDNAPRTIFIISMYSKDSQPRGM 60

QY 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIKDTKSDIIFQRSVPGHDKMQFESSY 120  
DB 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIKDTKSDIIFQRSVPGHDKMQFESSY 120

QY 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNE 157  
DB 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNE 157

RESULT 2  
AAY57570  
ID AAY57570 standard; protein; 157 AA.  
XX  
AC AAY57570;  
XX  
DT 06-MAR-2000 (first entry)  
XX  
DE Human interleukin 18 protein sequence SEQ ID NO:1.  
XX  
KW Human; interleukin 18; IL-18; potentiator; IGIF; tumour; cancer;  
KW interferon-gamma-inducing factor; growth inhibition; cytostatic.  
XX  
OS Homo sapiens.  
XX  
PN WO959565-A1.  
XX  
PD 25-NOV-1999.  
XX  
PF 20-MAY-1999; 99WO-US011160.  
XX  
PR 21-MAY-1998; 98US-0086560P.  
XX  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
XX  
PI Johnson RK;  
XX  
DR WPI; 2000-062368/05.  
XX  
PT New polypeptides, useful for preparation of composition for preventing  
PT and/or treating cancer by inhibiting tumor growth.  
XX  
PS Claim 1; Page 49-50; 53pp; English.  
XX  
CC The present sequence represents human interleukin 18 (IL-18). The present  
CC invention describes a compound comprising human or murine IL-18 in  
CC combination with a chemotherapeutic agent (1). Also described are: (1) a  
CC method of preventing and/or treating cancer in a mammal comprising the  
CC administration of a cancer inhibiting amount of (1) comprising the IL-18  
CC protein and the chemotherapeutic agent and optionally a pharmaceutically  
CC acceptable carrier; and (2) a method of inhibiting the growth of tumour  
CC cells in a mammal sensitive to a composition comprising human IL-18  
CC and/or murine IL-18 and the chemotherapeutic agent (and optionally a  
CC pharmaceutically acceptable carrier), comprising administering to a  
CC mammal afflicted with the tumour cells an effective tumour cell growth  
CC inhibiting amount of (1). The IL-18 protein in conjunction with a  
CC chemotherapeutic agent is useful in a method for preventing and/or  
CC treating cancer in mammals by inhibiting the growth of tumours or  
CC cancerous cells in mammals  
XX  
SQ Sequence 157 AA;

Query Match 99.9%; Score 811; DB 3; Length 157;  
Best Local Similarity 99.4%; Pred. No. 9.8e-83;  
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQNRPLFEDMTSDCRDNAPRTIFIISMYSKDSQPRGM 60

DB 1 YFGKLESKLSVIRNLNDQVLFIDQNRPLFEDMTSDCRDNAPRTIFIISMYSKDSQPRGM 60

QY 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIKDTKSDIIFQRSVPGHDKMQFESSY 120  
DB 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIKDTKSDIIFQRSVPGHDKMQFESSY 120

QY 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNE 157  
DB 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNE 157

RESULT 3  
AAG65351  
ID AAG65351 standard; protein; 157 AA.  
XX  
AC AAG65351;  
XX  
DT 30-NOV-2001 (first entry)  
XX  
DE Human interleukin-18 (IL-18) protein fragment.  
XX  
KW IL-18; interleukin-18; human; antibody; antirheumatic; cerebroprotective;  
KW neurotropic; neurological; antiinflammatory; antiparkinsonian; cardiant;  
KW immunosuppressive; antidepressant; neuroleptic; hepatotropic.  
XX  
OS Homo sapiens.  
XX  
PN WO200158956-A2.  
XX  
PD 16-AUG-2001.  
XX  
PF 09-FEB-2001; 2001WO-US004170.  
XX  
PR 10-FEB-2000; 2000US-0181608P.  
XX  
PA (BADI ) BASF AG.  
XX  
PI Ghayur T, Dixon RW, Roguska M, White M, Labkovsky B, Salfeld J,  
PI Duncan AR, Brocklehurst SM, Mankovich J, Shorrock CP, Thompson JE,  
PI Lennard SN;  
XX  
DR WPI; 2001-550020/61.  
XX  
PT Novel antibodies and compounds capable of binding to human interleukin-18  
PT useful for treating, e.g., inflammatory disorders, neurological  
PT disorders, heart failure, myocardial infarction, and autoimmune diseases.  
XX  
PS Disclosure; Page 14; 91pp; English.  
XX  
CC The invention provides isolated antibodies, or antigen-binding portions,  
CC that are capable of binding to human interleukin-18 (IL-18). The  
CC antibodies may be used to inhibit human IL-18 activity in, and treat a  
CC disorder where IL-18 is detrimental in, a human subject suffering from,  
CC inflammatory disorders (e.g., rheumatoid arthritis, Crohn's disease,  
CC inflammatory bowel disease, and osteoarthritis), neurological disorders  
CC (e.g., Huntington's chorea, Parkinson's disease, Alzheimer's disease, and  
CC stroke), heart failure, myocardial infarction, autoimmune diseases such  
CC as autoimmune hepatitis and autoimmune neuropenia, and mental disorders  
CC (e.g., depression and schizophrenia). Treatment with an anti-IL-18  
CC antibody may occur before, concurrent, or after administration of a  
CC second agent selected from an antibody, or fragment, capable of binding  
CC human IL-12, methotrexate, anti-tumor necrosis factor, corticosteroids,  
CC cyclosporin, rapamycin, FK506, and non-steroidal anti-inflammatory  
CC agents. The present sequence represents a human IL-18 protein fragment  
XX  
SQ Sequence 157 AA;

Query Match 99.9%; Score 811; DB 4; Length 157;  
Best Local Similarity 99.4%; Pred. No. 9.8e-83;  
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQNRPLFEDMTSDCRDNAPRTIFIISMYSKDSQPRGM 60

Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60  
 QY 61 AVTISVCKEKISLSCENKIIISFKEMNPPDNIKDTKSDIIFQORSVPGHDNKMOPESSY 120  
 Db 61 AVTISVCKEKISTSCENKIIISFKEMNPPDNIKDTKSDIIFQORSVPGHDNKMOPESSY 120  
 QY 121 EGYFLACKEKRDLPKLLKKEDELGDRSIMFTVQNE 157  
 Db 121 EGYFLACKEKRDLPKLLKKEDELGDRSIMFTVQNE 157

RESULT 4  
 AAG65294  
 ID AAG65294 standard; protein; 157 AA.  
 AC AAG65294;  
 XX  
 DT 30-NOV-2001 (first entry)  
 XX Human interleukin-18 (IL-18) protein fragment.  
 DE  
 XX IL-18; interleukin-18; human; antibody; antirheumatic; cerebroprotective;  
 KW nocropic; neurological; antiinflammatory; antiparkinsonian; cardiant;  
 KW immunosuppressive; antidepressant; neuroleptic; hepatotropic.  
 XX  
 OS Homo sapiens.  
 XX WO200158956-A2.  
 XX  
 PN 16-AUG-2001.  
 XX  
 PD  
 XX  
 PF 09-FEB-2001; 2001WO-US004170.  
 XX  
 PP 10-FEB-2000; 2000US-0181608P.  
 XX  
 PR (BADI ) BASF AG.  
 XX  
 PA Ghayur T, Dixon RW, Roguska M, White M, Labkovsky B, Salfeld J;  
 PI Duncan AR, Brocklehurst SM, Mankovich J, Shorrock CP, Thompson JE;  
 PI Lennard SN;  
 XX  
 DR WPI; 2001-550020/61.  
 XX  
 PT Novel antibodies and compounds capable of binding to human interleukin-18  
 PT useful for treating e.g., inflammatory disorders, neurological  
 PT disorders, heart failure, myocardial infarction, and autoimmune diseases.  
 XX  
 PS Disclosure; Page 9; 91pp; English.  
 XX  
 CC The invention provides isolated antibodies, or antigen-binding portions,  
 CC that are capable of binding to human interleukin-18 (IL-18). The  
 CC antibodies may be used to inhibit human IL-18 activity in, and treat a  
 CC disorder where IL-18 is detrimental in, a human subject suffering from,  
 CC inflammatory disorders (e.g., rheumatoid arthritis, Crohn's disease,  
 CC inflammatory bowel disease, and osteoarthritis), neurological disorders  
 CC (e.g., Huntington's chorea, Parkinson's disease, Alzheimer's disease, and  
 CC stroke), heart failure, myocardial infarction, autoimmune diseases such  
 CC as autoimmune hepatitis and autoimmune neutropenia, and mental disorders  
 CC (e.g., depression and schizophrenia). Treatment with an anti-IL-18  
 CC antibody may occur before, concurrent, or after administration of a  
 CC second agent selected from an antibody, or fragment, capable of binding  
 CC human IL-12, methotrexate, anti-tumor necrosis factor, corticosteroids,  
 CC cyclosporin, rapamycin, FK506, and non-steroidal anti-inflammatory  
 CC agents. The present sequence represents a human IL-18 protein fragment  
 XX  
 SQ Sequence 157 AA;  
 Query Match 99.9%; Score 811; DB 4; Length 157;  
 Best Local Similarity 99.4%; Pred. No. 9.8e-83;  
 Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60

Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60  
 QY 61 AVTISVCKEKISLSCENKIIISFKEMNPPDNIKDTKSDIIFQORSVPGHDNKMOPESSY 120  
 Db 61 AVTISVCKEKISTSCENKIIISFKEMNPPDNIKDTKSDIIFQORSVPGHDNKMOPESSY 120  
 QY 121 EGYFLACKEKRDLPKLLKKEDELGDRSIMFTVQNE 157  
 Db 121 EGYFLACKEKRDLPKLLKKEDELGDRSIMFTVQNE 157

RESULT 5  
 AAE06661  
 ID AAE06661 standard; protein; 157 AA.  
 AC AAE06661;  
 XX  
 DT 16-OCT-2001 (first entry)  
 XX Human interleukin-1gamma (IL-1gamma) protein.  
 DE  
 XX Human; interleukin-1gamma; IL-1gamma; virucide; hepatotropic; fever;  
 KW immunological disorder; tumour; inflammatory disorder; hypoglycaemia;  
 KW autoimmune disease; pulmonary tuberculosis; fulminant hepatitis; leprosy;  
 KW psoriasis; viral infection; allergy; cytokine; HIV; drug screening.  
 XX  
 OS Homo sapiens.  
 XX WO200157219-A2.  
 XX  
 PN 09-AUG-2001.  
 XX  
 PD  
 XX  
 PF 01-FEB-2001; 2001WO-US003285.  
 XX  
 PP 02-FEB-2000; 2000US-0179638P.  
 XX  
 PR (SCHE ) SCHERING CORP.  
 XX  
 PA Debets JEMA, Timans JC, Bazan JF, Kastelein RA;  
 PI WPI; 2001-488886/53.  
 XX  
 DR Novel isolated or recombinant antigenic interleukin-1 delta or epsilon  
 DR polypeptide useful for treating conditions exhibiting abnormal expression  
 PT of interleukin such as immunological disorders, tumor and allergy.  
 PT  
 XX Disclosure; Fig 1; 103pp; English.  
 PS  
 XX The invention relates to recombinant antigenic interleukin-1 like  
 CC molecules and their corresponding nucleic acid sequences, designated as  
 CC interleukin-1delta (IL-1delta) and interleukin-1epsilon (IL-1epsilon). IL  
 CC -1delta and IL-1epsilon are useful for treating conditions exhibiting  
 CC abnormal expression of the interleukin such as immunological disorders,  
 CC tumours, inflammatory disorders, fever, hypoglycaemia, psoriasis,  
 CC allergy, autoimmune diseases and infectious diseases (e.g., pulmonary  
 CC tuberculosis, leprosy, fulminant hepatitis, and viral infections such as  
 CC HIV). The invention also relates to methods of using the composition  
 CC containing IL-1delta or IL-1epsilon for both diagnostic and therapeutic  
 CC utilities. IL-1delta is used as an immunogen for the production of  
 CC antisera or antibodies specific, e.g., capable of distinguishing between  
 CC IL-1 family members and an IL-1delta, for the interleukin or its  
 CC fragment. The purified interleukin is used as a reagent to detect any  
 CC antibodies generated in response to the presence of elevated levels of  
 CC expression, or immunological disorders which lead to antibody production  
 CC to the endogenous cytokine. The invention also contemplates the use of  
 CC competitive drug screening assays. The present sequence is human  
 CC interleukin-1gamma (IL-1gamma) protein related to the invention  
 XX  
 SQ Sequence 157 AA;  
 Query Match 99.9%; Score 811; DB 4; Length 157;  
 Best Local Similarity 99.4%; Pred. No. 9.8e-83;

Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60  
 Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60

Qy 61 AVTISVKCEKISXLSCEKNKIIISFKEMNPPDNKOTKSDIIFQRSVPGHDNKMOPESSY 120  
 Db 61 AVTISVKCEKISTUSCENKIIISFKEMNPPDNKOTKSDIIFQRSVPGHDNKMOPESSY 120

Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157  
 Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 6  
 ID ABB04389  
 AC ABB04389 standard; protein; 157 AA.  
 XX ABB04389;  
 DT 21-MAY-2002 (first entry)  
 DE Human IL-18.  
 KW Human; IL-18; interleukin-18; cancer.  
 XX Homo sapiens.  
 FN CN1326992-A.  
 XX 19-DEC-2001.  
 PD 07-JUN-2000; 2000CN-00107993.  
 PF 07-JUN-2000; 2000CN-00107993.  
 PR (SHUA-) SHUANGLU PHARM CO LTD BEIJING.  
 PA Xu M, Wang Y, Huang X;  
 PI WPI; 2002-217571/28.  
 DR N-PSDB; ABL41315.  
 XX Gene cloning, product preparation and use of Chinese interleukin-18 subtype (53 Arg IL-18), useful for treating of cancer and other disease.  
 PT Claim 1; Page 7 (Disclosure); 8pp; Chinese.  
 PS The invention relates to the preparation of recombinant human interleukin -18 for treating of cancer and other disease  
 CC Sequence 157 AA;

Query Match 99.9%; Score 811; DB 5; Length 157;  
 Best Local Similarity 99.4%; Pred. No. 9.8e-83;  
 Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60  
 Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60

Qy 61 AVTISVKCEKISXLSCEKNKIIISFKEMNPPDNKOTKSDIIFQRSVPGHDNKMOPESSY 120  
 Db 61 AVTISVKCEKISTUSCENKIIISFKEMNPPDNKOTKSDIIFQRSVPGHDNKMOPESSY 120

Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157  
 Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 7  
 ID AAE17134

ID AAE17134 standard; protein; 157 AA.  
 XX AAE17134;  
 AC 22-APR-2002 (first entry)  
 DT Human IL-18 protein.  
 DE Human; viral disease; IL-18; interferon-gamma-inducing factor; IGIF; HSV; influenza virus; human immunodeficiency virus; HIV; herpes simplex virus; hepatitis A virus; HAV; hepatitis B virus; HBV; human papillomavirus; HPV; hepatitis C virus; HCV.  
 KW Homo sapiens.  
 XX WO200193898-A1.  
 FN 13-DEC-2001.  
 PD 01-JUN-2001; 2001WO-US017924.  
 PF 02-JUN-2000; 2000US-0208869P.  
 PR (SMIK ) SMITHKLINE BEECHAM CORP.  
 PA Esser KM, Rosenberg M, Tal-Singer R, Woodnutt G, Chisari FV;  
 PI WPI; 2002-154554/20.  
 DR Treatment of disease caused by e.g. influenza virus comprises administration of composition containing polypeptide, having identity of amino acid sequences.  
 XX Claim 1; Fig 1; 4lpp; English.  
 XX The invention relates to a method for treating viral diseases with IL-18, also known as interferon-gamma-inducing factor (IGIF) and IL-18 combinations. The method involves administering a composition comprising IL-18 and IL-18 in combination with other agents. The method is used for treating diseases caused by viruses such as influenza virus, human immunodeficiency virus (HIV), herpes simplex virus (HSV), hepatitis A virus (HAV), hepatitis B virus (HBV), human papillomavirus (HPV) and hepatitis C virus (HCV). The present sequence is human IL-18 protein

Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60  
 Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60

Qy 61 AVTISVKCEKISXLSCEKNKIIISFKEMNPPDNKOTKSDIIFQRSVPGHDNKMOPESSY 120  
 Db 61 AVTISVKCEKISTUSCENKIIISFKEMNPPDNKOTKSDIIFQRSVPGHDNKMOPESSY 120

Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157  
 Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 8  
 ID AAE16954  
 AC AAE16954 standard; protein; 157 AA.  
 XX AAE16954;  
 DT 18-APR-2002 (first entry)  
 DE Human active interleukin-18 (IL-18) protein.

KW Human; interleukin-18; IL-18; caspase; interferon gamma; IFN-gamma;  
KW immunocompetent.  
XX Homo sapiens.  
OS WO200198455-A2.  
PN 27-DEC-2001.  
XX 11-JUN-2001; 2001WO-US018804.  
XX 15-JUN-2000; 2000US-0211832P.  
PR 10-AUG-2000; 2000US-0224128P.  
PR 20-JAN-2001; 2001US-0264923P.  
XX (SMIK ) SMITHLINE BEECHAM CORP.  
XX  
XX Johanson KO, Kirkpatrick RB, Shatzman AR, Hoy YS, Mcdevitt P;  
XX WPI; 2002-139786/18.  
DR  
XX Activation of precursor polypeptide e.g. interleukin-18 polypeptide  
PT useful for inducing interferon-gamma production, comprises contacting or  
PT co-expressing caspase 4 or caspase 5 with precursor polypeptide.  
XX  
XX Claim 9; Fig 3; 64pp; English.  
PS  
XX The invention relates to a method for the in vitro activation of human  
CC precursor interleukin-18 (Pro-IL-18) with an activating enzyme. The  
CC method comprises contacting precursor IL-18 with an activating enzyme  
CC such as caspase 4 or caspase 5. Caspases 4 and 5 are members of a family  
CC of cysteine proteases that include interleukin-1beta converting enzyme  
CC (ICE), which preferentially cleave substrates containing a protease  
CC activation motif. The methods are useful for producing physiologically  
CC active polypeptide e.g. active IL-18 polypeptide. The active IL-18  
CC polypeptide has an activity of inducing the production of interferon  
CC (IFN)-gamma in immunocompetent cells. IFN-gamma is useful as a  
CC biologically active substance for stimulating the production of IFNg from  
CC KG-1 (human myelomonocytic cell line) cells. The present sequence is  
CC human active IL-18 protein  
XX  
SQ Sequence 157 AA;  
  
Query Match 99.9%; Score 811; DB 5; Length 157;  
Best Local Similarity 99.4%; Pred. No. 9.8e-83;  
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60  
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60  
  
QY 61 AVTISVCKEKISLSCENKIISFKEMNPPDNKOTKSDIIFQRSVPVGHDKMQFESSY 120  
DB 61 AVTISVCKEKISLSCENKIISFKEMNPPDNKOTKSDIIFQRSVPVGHDKMQFESSY 120  
  
QY 121 EGYFLACEKERDLFKLLILKKEDELGDRSIMFTVQNEED 157  
DB 121 EGYFLACEKERDLFKLLILKKEDELGDRSIMFTVQNEED 157  
  
RESULT 9  
ABG73359  
ID ABG73359 standard; protein; 157 AA.  
XX  
AC ABG73359;  
XX  
DT 13-MAY-2003 (first entry)  
XX  
DE Human wild-type mature interleukin-18 (IL-18).  
XX Human; human interleukin-18; IL-18; IL-18 binding protein; IL-18BP;  
KW T helper type I response; Th1 response; cancer; viral disease;  
KW microbial infection; tumour immunotherapy; adjuvant; DNA vaccination;

KW graft versus tumour therapy; neutralisation; cytostatic; virucide;  
KW antimicrobial.  
XX Homo sapiens.  
OS US2002169291-A1.  
PN 14-NOV-2002.  
XX 08-MAR-2002; 2002US-00094153.  
XX 08-MAR-2001; 2001US-0274327P.  
XX (DINA/) DINARELLO C.  
PA (KIMS/) KIM S H.  
XX Dinarello C, Kim SH;  
PI WPI; 2003-298731/29.  
XX N-PSDB; ABX11788.  
DR  
XX Novel interleukin-18 mutant polypeptide useful in the treatment of cancer  
PT and viral disease, has mutations in amino acid residues which are  
PT involved in its interaction with IL-18 binding protein.  
XX  
XX Example 1; Fig 1B; 23pp; English.  
PS  
XX The present invention relates to mutants of human interleukin-18 (IL-18)  
CC protein that have a lower affinity for IL-18 binding protein (IL-18BP)  
CC than the wild-type IL-18 protein. The IL-18 mutants of the invention  
CC comprise mutations in one or more amino acid residues which are involved  
CC in its interaction with IL-18BP. The mutations comprise substitutions,  
CC preferably non-conservative, additions or deletions. A pharmaceutical  
CC composition comprising an IL-18 mutant is useful for treating a disease  
CC which is prevented or alleviated by a T helper type I (Th1) response,  
CC including cancer and viral disease. The IL-18 mutants are useful in the  
CC treatment of the above diseases, microbial infections, in tumour  
CC immunotherapy, and as an adjuvant in DNA vaccination and in graft versus  
CC tumour therapy. The IL-18 mutants are resistant to, or less susceptible  
CC to, neutralisation than the wild-type protein. The present sequence  
CC represents human wild-type mature IL-18 protein  
XX  
SQ Sequence 157 AA;  
  
Query Match 99.9%; Score 811; DB 6; Length 157;  
Best Local Similarity 99.4%; Pred. No. 9.8e-83;  
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60  
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60  
  
QY 61 AVTISVCKEKISLSCENKIISFKEMNPPDNKOTKSDIIFQRSVPVGHDKMQFESSY 120  
DB 61 AVTISVCKEKISLSCENKIISFKEMNPPDNKOTKSDIIFQRSVPVGHDKMQFESSY 120  
  
QY 121 EGYFLACEKERDLFKLLILKKEDELGDRSIMFTVQNEED 157  
DB 121 EGYFLACEKERDLFKLLILKKEDELGDRSIMFTVQNEED 157  
  
RESULT 10  
ADA50616  
ID ADA50616 standard; protein; 157 AA.  
XX  
AC ADA50616;  
XX  
DT 20-NOV-2003 (first entry)  
XX  
DE Human mature consensus interleukin-18 (IL-18), SEQ ID NO:71.  
XX Nucleic acid vaccine; DNA vaccine; tumour antigen; cytokine adjuvant;  
KW humoral response; cellular response; immune response; immunotherapy;



protein. A variant protein with this substitution would have changed activity compared to the wild-type protein"  
111  
/note= "Lys may replace wild-type Asn in a variant protein. A variant protein with this substitution would have changed activity compared to the wild-type protein"  
129  
/note= "Phe may replace wild-type Lys in a variant protein. A variant protein with this substitution would have changed activity compared to the wild-type protein"  
131  
/note= "Asp may replace wild-type Arg in a variant protein. A variant protein with this substitution would have changed activity compared to the wild-type protein"  
132  
/note= "Leu may replace wild-type Asp in a variant protein. A variant protein with this substitution would have changed activity compared to the wild-type protein"  
133  
/note= "Glu may replace wild-type Leu in a variant protein. A variant protein with this substitution would have changed activity compared to the wild-type protein"  
134  
/note= "Ala may replace wild-type Phe in a variant protein. A variant protein with this substitution would have changed activity compared to the wild-type protein"

WO2003031569-A2.

17-APR-2003.

18-SEP-2002; 2002WO-US029640.

10-OCT-2001; 2001US-0328371P.

(CENZ ) CENTOCOR INC.

Snyder L, Scallan B, Knight DM, McCarthy SG, Goletz TJ; Branigan PJ;

WPI; 2003-393437/37.  
N-PSDB; ADA50613.

New nucleic acid vaccine, useful for eliciting an immune response to a

Query Match 99.9%; Score 811; DB 6; Length 157;  
Best Local Similarity 99.4%; Pred. No. 9.8e-83;  
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYSKDSQPRGM 60

DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYSKDSQPRGM 60

QY 61 AVTISVKCEKISXLSCEKNKIIISFKEMNPPDNKDKSDIIFQRSVPVGHNDKMQFESSY 120

DB 61 AVTISVKCEKISTLSCENKIIISFKEMNPPDNKDKSDIIFQRSVPVGHNDKMQFESSY 120

QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 11

ADA50610 standard; protein; 157 AA.

XX AC ADA50610;

XX DT 20-NOV-2003 (first entry)

XX DE Human mature consensus interleukin-18 (IL-18), SEQ ID NO:65.

XX KW Nucleic acid vaccine; DNA vaccine; tumour antigen; cytokine adjuvant;

KW humoral response; cellular response; immune response; immunotherapy;  
KW cancer; cytostatic; vaccine; gene therapy; interleukin-18; IL-18; human.  
XX Homo sapiens.  
OS WO2003031569-A2.  
FN 17-APR-2003.  
PD 18-SEP-2002; 2002WO-US029640.  
PF 10-OCT-2001; 2001US-0328371P.  
PR (CENZ ) CENTOCOR INC.  
PA Snyder L, Scallan B, Knight DM, McCarthy SG, Goletz TJ;  
PI Branigan PJ;  
XX WPI; 2003-393437/37.  
DR N-PSDB; ADA50608.  
XX New nucleic acid vaccine, useful for eliciting an immune response to a  
PT cancer associated tumor protein in a mammal.  
FT Claim 1b; Page 51-52; 92pp; English.  
XX The invention relates to a nucleic acid vaccine comprising one or more  
CC tumour antigen-encoding nucleic acids and one or more cytokine adjuvant-  
CC encoding nucleic acids. The tumour antigen encoded by the vaccine is  
CC mucin 1 (MUC-1), the kallikrein KUK2, or prostate specific antigen (PSA,  
CC also known as KLK3), and the cytokine adjuvant encoded can be interleukin  
CC -12 (IL-12), granulocyte macrophage-colony stimulating factor (GM-CSF),  
CC or especially interleukin-18 (IL-18). The antigen-encoding nucleic acid  
CC is preferably under the control of a promoter such as the cytomegalovirus  
CC immediate early promoter, the dihydrofolate reductase promoter or the  
CC early or late SV40 promoters. The invention also encompasses the method  
CC of eliciting an immune response to a tumour antigen in a mammal using the  
CC vaccine of the invention. Coexpression of the antigen and adjuvant  
CC induces a humoral or cellular response to the tumour antigen, generating  
CC an immune response useful for treatment or prophylaxis of cancers. The  
CC present sequence represents an interleukin-18 (IL-18) polypeptide which  
CC is specifically claimed for use in the vaccine of the invention.  
XX

Sequence 157 AA;

Query Match 99.9%; Score 811; DB 6; Length 157;  
Best Local Similarity 99.4%; Pred. No. 9.8e-83;  
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYSKDSQPRGM 60

DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYSKDSQPRGM 60

QY 61 AVTISVKCEKISXLSCEKNKIIISFKEMNPPDNKDKSDIIFQRSVPVGHNDKMQFESSY 120

DB 61 AVTISVKCEKISTLSCENKIIISFKEMNPPDNKDKSDIIFQRSVPVGHNDKMQFESSY 120

QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 12

ABR83372 standard; protein; 157 AA.

XX AC ABR83372;

XX DT 07-OCT-2003 (first entry)

XX DE Human interleukin 18 amino acid sequence.

XX KW Human; interleukin 1; IL-1; interleukin 18; IL-18; mutant; mutein;

KW mutant interleukin 18; MUT-IL-18; antiinflammatory; gene therapy;  
KW inflammatory disorder.

XX Homo sapiens.

XX WO2003057821-A2.

XX 17-JUL-2003.

XX 25-OCT-2002; 2002WO-US034235.

XX 26-OCT-2001; 2001US-0335880P.

XX (CENZ ) CENTOCOR INC.

XX Heavner GA, Snyder LA, Mccarthy SG;

XX WPI; 2003-577517/54.

XX New MUT-IL-18 nucleic acid, useful for preparing a composition for  
PT diagnosing or treating a MUT-IL-18 related condition, e.g., inflammatory  
PT disorder.

XX Example 3; Page 74; 97pp; English.

XX The present invention describes a mutant interleukin 18 (MUT-IL-18)  
CC nucleic acid comprising or complementary to at least one polynucleotide  
CC encoding an IL-18 amino acid sequence comprising at least one mutation  
CC corresponding to at least one substitution selected from the group  
CC consisting of Thr10 for Ser10, Val12 for Ile12, Ser45 for Thr47  
CC for Phe47, Phe52 for Tyr52, Val64 for Ile64, Tyr101 for Phe101, Val5 for  
CC Leu5, Val20 for Leu20, Ile20 for Leu20, Tyr21 for Phe21, Val22 for Ile22,  
CC Ile66 for Val66, Thr72 for Ser72, or Phe48 for Ser148. Also described:  
CC (1) a MUT-IL-18 polypeptide; (2) a MUT-IL-18 antibody; (3) a MUT-IL-18  
CC vector comprising the MUT-IL-18 nucleic acid; (4) a MUT-IL-18 host cell  
CC comprising the MUT-IL-18 nucleic acid; (5) a composition comprising a MUT  
CC -IL-18 nucleic acid, polypeptide or antibody; (6) diagnosing or treating  
CC a MUT-IL-18 related condition in a cell, tissue, organ or animal; (7) a  
CC device comprising MUT-IL-18 nucleic acid, polypeptide or antibody and  
CC that is suitable for contacting or administering the MUT-IL-18 nucleic  
CC acid, polypeptide or antibody; (8) an article of manufacture for human  
CC pharmaceutical or diagnostic use; and (9) producing the MUT-IL-18 nucleic  
CC acid, polypeptide or antibody. MUT-IL-18 has antiinflammatory activity  
CC and can be used in gene therapy. The MUT-IL-18 nucleic acid can be used  
CC for preparing a composition for diagnosing or treating a MUT-IL-18  
CC related condition, e.g., inflammatory disorder. The present sequence  
CC represents a human IL-18 amino acid sequence given in an example from the  
CC present invention

XX Sequence 157 AA;

Query Match 99.9%; Score 811; DB 6; Length 157;

Best Local Similarity 99.4%; Pred. No. 9.8e-83;

Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIIISMYKDSQPRGM 60

Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIIISMYKDSQPRGM 60

Qy 61 AVTISVKCEKISLSCENKIIISFKEMNPPDNIKOTKSDIIFQRSVPGHDKNMQPESSSY 120

Db 61 AVTISVKCEKISTLSCENKIIISFKEMNPPDNIKOTKSDIIFQRSVPGHDKNMQPESSSY 120

Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 13

ADE06775

ID ADE06775 standard; protein; 157 AA.

XX

AC ADE06775;

XX 29-JAN-2004 (first entry)

XX Human anti-diabetes Ig derived protein SEQ ID NO:3.

XX human; Ig; diabetes; complementarity-determining region; CDR;

XX antidiabetic; ophthalmological; neuroprotective; gene therapy;

XX diabetes mellitus; insulin resistance; hyperglycaemia; hypoglycaemia;

XX pancreatitis; Cushing's syndrome; acanthosis nigricans; retinopathy;

XX nephropathy; polyneuropathy; ulcer; infection.

XX Homo sapiens.

XX WO2003083071-A2.

XX 09-OCT-2003.

XX 26-MAR-2003; 2003WO-US009459.

XX 26-MAR-2002; 2002US-0367902P.

XX (CENZ ) CENTOCOR INC.

XX Griswold DE, Li J, Li L;

XX WPI; 2003-804047/75.

XX New isolated anti-diabetes immunoglobulin (Ig)-derived protein,  
PT comprising at least one complementarity determining region (CDR) useful  
PT for treating a diabetes-related condition, e.g. type I or II diabetes  
PT mellitus, retinopathy.

XX Claim 1; SEQ ID NO 3; 84pp; English.

XX The invention relates to a novel isolated anti-diabetes immunoglobulin  
CC (Ig)-derived protein, comprising at least one complementarity-determining  
CC region (CDR). A protein of the invention has antidiabetic.

CC ophthalmological, and neuroprotective activity, and may have a use in  
CC gene therapy. The protein, nucleic acid, composition and methods of the  
CC invention are useful for treating a diabetes-related condition, e.g. type  
CC I or II diabetes mellitus, insulin resistance, hyperglycaemia,

CC hypoglycaemia, pancreatitis, Cushing's syndrome, acanthosis nigricans,

CC retinopathy, nephropathy, polyneuropathy, ulcers, or infections. The

CC present sequence represents an anti-diabetes Ig derived protein of the

CC invention.

XX Sequence 157 AA;

Query Match 99.9%; Score 811; DB 7; Length 157;

Best Local Similarity 99.4%; Pred. No. 9.8e-83;

Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIIISMYKDSQPRGM 60

Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIIISMYKDSQPRGM 60

Qy 61 AVTISVKCEKISLSCENKIIISFKEMNPPDNIKOTKSDIIFQRSVPGHDKNMQPESSSY 120

Db 61 AVTISVKCEKISTLSCENKIIISFKEMNPPDNIKOTKSDIIFQRSVPGHDKNMQPESSSY 120

Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 14

AAY85167

ID AAY85167 standard; protein; 158 AA.

XX

AC AAY85167;

XX 23-JUN-2000 (first entry)

XX



```
DE Human interleukin-18 (IL-18) amino acid sequence.
XX
KW Interleukin-18; production; IL-18; human; medical injection product.
XX
OS Homo sapiens.
XX
PN CN1243130-A.
XX
PD 02-FEB-2000.
XX
PF 24-JUL-1998; 98CN-00103307.
XX
PR 24-JUL-1998; 98CN-00103307.
XX
PA (WUGG/) WU G.
XX
PI Wu G, Liu Z;
XX
WPI; 2000-340020/30.
DR N-PSDB; AAA10526.
XX
PT Preparation method for engineering bacteria for recombination of human
PT leucocyte medium-18 and its product thereof.
XX
PS Claim 1; Page 2; 17pp; English.
XX
CC This sequence represents the human interleukin-18 (IL-18) amino acid
CC sequence. The invention relates to a method for engineering bacterium for
CC recombination of human IL-18 and a method for the preparation of IL-18. A
CC primer containing a restriction endonuclease site can be used to
CC accurately obtain the IL-18 gene containing 474 nucleotides, and uses the
CC stop codon preferred by coli bacillus to raise the expression rate. The
CC method uses a high-amplification culture medium to increase the
CC expression level and only requires a one-step purification process to
CC obtain a medical injection-pure product
XX
SQ Sequence 158 AA;
Query Match 99.9%; Score 811; DB 3; Length 158;
Best Local Similarity 99.4%; Pred. No. 9.9e-83;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYSKDSQPRGM 60
DB 2 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYSKDSQPRGM 61
QY 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIKDTKSDIIFQRSVPVGHDKNQPFESSY 120
DB 62 AVTISVKCEKISLSCENKIISFKEMNPPDNIKDTKSDIIFQRSVPVGHDKNQPFESSY 121
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
DB 122 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 158
RESULT 15
ADA50614
ID ADA50614 standard; protein; 177 AA.
XX
AC ADA50614;
XX
DT 20-NOV-2003 (first entry)
XX
DE Mature consensus IL-18/ILC signal sequence fusion protein, SEQ ID NO:69.
XX
KW Nucleic acid vaccine; DNA vaccine; tumour antigen; cytokine adjuvant;
KW humoral response; cellular response; immune response; immunotherapy;
KW cancer; cytostatic; vaccine; gene therapy; interleukin-18; IL-18; human.
XX
OS Chimeric.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..20
FT Protein /label= Human_LC_signal_sequence
FT 21..177
FT /label= Mature_consensus_IL-18
XX
PN WO2003031569-A2.
XX
PD 17-APR-2003.
XX
PF 18-SEP-2002; 2002WO-US029640.
XX
PR 10-OCT-2001; 2001US-0328371P.
XX
PA (CENZ ) CENTOCOR INC.
XX
PI Snyder L, Scallan B, Knight DM, Mccarthy SG, Goletz TJ;
PI Branigan PJ;
XX
WPI; 2003-393437/37.
DR N-PSDB; ADA50611.
XX
PT New nucleic acid vaccine, useful for eliciting an immune response to a
PT cancer associated tumor protein in a mammal.
XX
PS Claim 1b; Page 53; 92pp; English.
XX
CC The invention relates to a nucleic acid vaccine comprising one or more
CC tumour antigen-encoding nucleic acids and one or more cytokine adjuvant-
CC encoding nucleic acids. The tumour antigen encoded by the vaccine is
CC mucin 1 (MUC-1), the kallikrein KUK2, or prostate specific antigen (PSA,
CC also known as KLK3), and the cytokine adjuvant encoded can be interleukin
CC -12 (IL-12), granulocyte macrophage-colony stimulating factor (GM-CSF),
CC or especially interleukin-18 (IL-18). The antigen-encoding nucleic acid
CC is preferably under the control of a promoter such as the cytomegalovirus
CC immediate early promoter, the dihydrofolate reductase promoter or the
CC early or late SV40 promoters. The invention also encompasses the method
CC of eliciting an immune response to a tumour antigen in a mammal using the
CC vaccine of the invention. Coexpression of the antigen and adjuvant
CC induces a humoral or cellular response to the tumour antigen, generating
CC an immune response useful for treatment or prophylaxis of cancers. The
CC present sequence represents an interleukin-18 (IL-18) polypeptide which
CC is specifically claimed for use in the vaccine of the invention.
XX
SQ Sequence 177 AA;
Query Match 99.9%; Score 811; DB 6; Length 177;
Best Local Similarity 99.4%; Pred. No. 1.2e-82;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYSKDSQPRGM 60
DB 21 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYSKDSQPRGM 80
QY 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIKDTKSDIIFQRSVPVGHDKNQPFESSY 120
DB 81 AVTISVKCEKISLSCENKIISFKEMNPPDNIKDTKSDIIFQRSVPVGHDKNQPFESSY 140
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
DB 141 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 177
Search completed: August 19, 2004, 13:35:04
Job time : 54 secs
```

**This Page Blank (uspto)**

A;Gene: SPDB:SPBC3B9.02c

A,Map position: 2

Query Match 10.5%; Score 85; DB 2; Length 381;  
Best Local Similarity 26.4%; Pred. No. 1.6;  
Matches 39; Conservative 23; Mismatches 54; Indels 32; Gaps 7;  
QY 3 GKLESKLVIRNLNDQVLFIDQGNRPFLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGMV 62  
DB 208 QQLSSKDAF--DVNQRPTFLGMAKPVDSSELTDFIWNPKTKMF----- 250  
QY 63 TISVK-CEKISXLSCEKIIISF-KEMNPPDNIKDTKSDIIFQRSVPGHDKMQPFESSY 120  
DB 251 -LPVKPLESNGALNSQNEHTEVQKKSIDNL--TFSSSELPKRS--RDNNLSSESS-- 302  
QY 121 EGYFLACEKERDLFKLILKKEDELGDRS 148  
DB 303 -----VSSKHLIDYNSRNYNKRDRDPRT 325

RESULT 3  
T39487  
hypotheical protein SPBC15D4.11c - fission yeast (Schizosaccharomyces pombe)  
C:Species: Schizosaccharomyces pombe  
C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 04-Mar-2000  
C:Accession: T39487  
R:Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Lucas, M.; Gaillardin, C.  
submitted to the EMBL Data Library, August 1997  
A:Reference number: 221858  
A:Accession: T39487  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-263 <LYN>  
A:Cross-references: EMBL:AL013149; PIDN:CAA20486.2; GSPDB:GN00067; SPDB:SPBC15D4.11c  
A:Experimental source: strain 972h; cosmid c15D4  
C:Genetics:  
A:Gene: SPDB:SPBC15D4.11c  
A:Map position: 2  
A:Introns: 96/2; 147/3  
C:Superfamily: Schizosaccharomyces pombe hypothetical protein SPBC15D4.11c

Query Match 10.1%; Score 82; DB 2; Length 263;  
Best Local Similarity 21.7%; Pred. No. 2;  
Matches 35; Conservative 33; Mismatches 65; Indels 28; Gaps 5;  
QY 4 KLESKLVIRNLNDQVLFIDQGNRPFLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGMV 63  
DB 47 KLDSELGVYKQVLDLTPKKGYEKALHSFIHED-----PSLNYISALKETAKERIRVT 100  
QY 64 ISVKCEKISXLSCEKIIISF-KEMNPPDNIKDTKSDIIFQRSVPGH----- 109  
DB 101 VPVYSSRKSYV--QTKPIITHGAEN--ENGNETSDLVFFQHSIPAYVQLTNNHGTILCAL 156  
QY 110 ---DNKMQPFESSSYEGYFLACEKERDLFKLILKKEDELGDR 147  
DB 157 ILCKGMLHFDLSIFSQSPQNSQAFSSDL-RLILQKSQKVTGR 196

RESULT 4  
S10532  
interleukin-1 alpha precursor - pig  
N:Alternate names: hematopoietin-1; IL-1 alpha  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 20-Feb-1995 #sequence\_revision 22-Nov-1996 #text\_change 28-Jan-2000  
C:Accession: S10532  
R:Maliszewski, C.R.; Renshaw, B.R.; Schoenborn, M.A.; Urban, J.F.; Baker, P.E.  
Nucleic Acids Res. 18, 4282, 1990  
A:Title: Porcine IL-1 alpha cDNA nucleotide sequence.  
A:Reference number: S10532; MUID:90332454; PMID:2377484  
A:Accession: S10532  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-270 <MAL>  
A:Cross-references: EMBL:X52731; NID:g1987; PIDN:CAA36945.1; PID:g1988

C;Comment: Produced by activated macrophages, the IL-1 proteins stimulate thymocyte proliferation.  
C;Comment: IL-1 proteins are involved in the inflammatory response, being identified as a form of interleukin-1alpha, unlike interleukin-1beta, is fully active.

C;Superfamily: interleukin-1  
C;Keywords: cytokine; immunoregulation; inflammation; lipoprotein; lymphokine; macrophage F;112/Domain: propeptide #status predicted <PRO>  
F;113-270/Product: interleukin-1 alpha #status predicted <IL1>  
F;82.83/Binding site: myristate (Lys) (covalent) #status predicted

Query Match 10.0%; Score 81.5; DB 1; Length 270;  
Best Local Similarity 22.7%; Pred. No. 2.3;  
Matches 30; Conservative 32; Mismatches 57; Indels 13; Gaps 6;

QY 8 KLSVIRNLNDQVLFIDQGNRPFLFEDMTD-----SDCRDNAPRTI-FIISMYKDSQPRGMV 62  
DB 123 KYNFMRVINHQICILNDARNQSIIRDPSQYLMAAVLNLDKAVKEDMAAYTSNDDSQLPV 182  
QY 63 TISVKCEKISXLSCEK--KIISFKEM-NPPDNIKDTKSDIIFQRSVPGHDKMQPFESS 119  
DB 183 TLRIS-ETRLFVSAQNEDEPVLLKELPPTKTKIDETSLLPFWEK---HGNMDYFKSAA 237  
QY 120 YEGYFLACEKER 131  
DB 238 HPKLFIFATROBK 249

RESULT 5  
C71509  
probable DNA polymerase I - Chlamydia trachomatis (serotype D, strain UW3/Cx)  
C:Species: Chlamydia trachomatis  
C:Date: 13-Sep-1998 #sequence\_revision 13-Sep-1998 #text\_change 08-Oct-1999  
C:Accession: C71509  
R:Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, Science 282, 754-759, 1998  
A:Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis  
A:Reference number: A71570; MUID:99000809; PMID:9784136  
A:Accession: C71509  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-866 <ARN>  
A:Cross-references: GB:AE001322; GB:AE001273; NID:g3328916; PIDN:AAC68093.1; PID:g3328922  
A:Experimental source: serotype D, strain UW-3/Cx  
C:Genetics:  
A:Gene: polA  
C:Superfamily: DNA-directed DNA polymerase I

Query Match 9.9%; Score 80.5; DB 2; Length 866;  
Best Local Similarity 26.4%; Pred. No. 11;  
Matches 34; Conservative 22; Mismatches 28; Indels 45; Gaps 8;

QY 1 YFGKLESKLVIRNLNDQVLFI---DQGNRPFLFEDMTD-----SDCRDNAPRTIFI 49  
DB 441 YFGMLASKLAIKN-----YLFVKLEEKGLKIDIFEVEQPLEAVLFAMEC-----V 486

QY 50 SMYKDSQPRGMV---TISVKCEKIS-----XLSCEKIIISFKEMN-----PPDN 91  
DB 487 GMPLDSQ--GLAVLDRDLTKLEECSEQEIYDLVGCEFNKSPKQLSDILYQRLGIEPVDK 544  
QY 92 IKOTKSDII 100  
DB 545 AKSTKAEVL 553

RESULT 6  
D64583  
hypothetical protein HP0508 - Helicobacter pylori (strain 26695)  
C:Species: Helicobacter pylori  
C:Date: 09-Aug-1997 #sequence\_revision 09-Aug-1997 #text\_change 08-Oct-1999  
C:Accession: D64583  
R:Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.;

Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenna, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997  
A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpik, P.D.; Smith, H.O.; Fraser, C.  
A:Title: The complete genome sequence of the gastric pathogen *Helicobacter pylori*.  
A:Reference number: A64520; MUID:97394467; PMID:9252185  
A:Accession: D64583  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-452 <TOM>  
A:Cross-references: GB:AE000565; GB:AE000511; NID:92313616; PIDN:AAD07578.1; PID:9231362

Query Match 9.7%; Score 79; DB 2; Length 452;  
Best Local Similarity 23.8%; Pred. No. 7.4;  
Matches 40; Conservative 30; Mismatches 72; Indels 26; Gaps 8;

Qy 9 LSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSOPR----- 58  
Db 105 LVYFRQFNQA-FLIAPNDELYEQIRATNTDINFISDLLVTLFNGFDPFKIANLRKACNV 163

Qy 59 -GMATVISVCKEISLSCEN-KIISFKEMNPPDNIKDTKSDIIFQFORSVPGHD-----NK 112  
Db 164 YSVGVYIVVTNTNLISCFEILEKREL---DTSGVTKSTPTFSR-VEGIDAGTLGK 219

Qy 113 MQPSSSYEGYF----LACEKRDLFKILKKEDELGRSIMFTVQNE 156  
Db 220 L-FSGSQSKNFAYVDALVKKKREKREVKRIKKEIKDSIKREIKQE 266

RESULT 7  
T44357  
hypothetical protein [imported] - Clostridium histolyticum  
C:Species: Clostridium histolyticum  
C:Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 21-Jul-2000  
C:Accession: T44357  
R:Matsushita, O.; Jung, C.M.; Katayama, S.; Minami, J.; Takahashi, Y.; Okabe, A.  
J. Bacteriol. 181, 923-933, 1999  
A:Title: Gene duplication and multiplicity of collagenases in Clostridium histolyticum.  
A:Reference number: 222752; MUID:99121032; PMID:9922257

A:Accession: T44357  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-204 <MAT>  
A:Cross-references: EMBL:AB014075; NID:93868863; PIDN:BAA34544.1; PID:93892648  
A:Experimental source: strain JCM 1403

Query Match 9.7%; Score 78.5; DB 2; Length 204;  
Best Local Similarity 26.4%; Pred. No. 3.2;  
Matches 32; Conservative 19; Mismatches 51; Indels 19; Gaps 5;

Qy 9 LSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSOPRGMATVTSV 66  
Db 25 ISTFENRHHKASSNKQGAKEKIN-----IDNSNSIKIVESVILKPEGEQNKYTVDE 80

Qy 67 KCEK-----ISXLSCKENKIISFKEMNPPDNIKDTKSDIIFQFORSVPGHNMQFSSS 119  
Db 81 CIEKFNKDKVSDMTKEQVLAVFKHD--YNLKDIKKDQIVFSRSI-----NKYKQSEK 134

Qy 120 Y 120  
Db 135 Y 135

RESULT 8  
T32038  
hypothetical protein F41B5.2 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 16-Feb-2001  
C:Accession: T32038  
R:Dante, M.; Kramer, J.  
submitted to the EMBL Data Library, July 1997  
A:Description: The sequence of C. elegans cosmid F41B5.  
A:Reference number: Z21115

A:Accession: T32038  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-473 <DAN>  
A:Cross-references: EMBL:AF016676; PIDN:AAC25900.1; GSPDB:GN00023; CESP:F41B5.2  
A:Experimental source: strain Bristol N2; clone F41B5  
C:Genetics:  
A:Gene: CESP:F41B5.2  
A:Map position: 5  
A:Introns: 67/1; 233/2; 403/3  
C:Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology  
C:Keywords: heme; iron; metalloprotein  
F:298-461/Domain: cytochrome P450 homology <P45>  
F:439/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 9.6%; Score 78; DB 2; Length 473;  
Best Local Similarity 21.5%; Pred. No. 9.7;  
Matches 32; Conservative 28; Mismatches 57; Indels 32; Gaps 6;

Qy 10 SVIRNLNDQVLF----IDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSOPRGMATVTSV 66  
Db 170 NAIANVINQITIFGYRFDSESNQBEYKKLKH-----LIEFQENVFTSAKVTQV 216

Qy 67 KCEKISXLSCKENKIISFKEMNPPDNIKDTKSDIIFQFORSVPGHNMQFSSSYEGYPL 125  
Db 217 FAPKL-----GKILPGESLE--DLMKDWKNSFYDFNTQIENHRQKIDFDSSESQDYAE 268

Qy 126 ACEKRDLFKILKKEDELGRSIMFTVQ 154  
Db 269 AYLKEQ-----KKYEALGDTLFSNKQ 290

RESULT 9  
A56677  
neuronal cell cycle withdrawal protein QN1 - quail (fragment)  
C:Species: Coturnix coturnix (quail)  
C:Date: 21-Jul-1995 #sequence\_revision 28-Jul-1995 #text\_change 21-Jul-2000  
C:Accession: A56677  
R:Bidou, L.; Crisanti, P.; Blancher, C.; Peseac, B.  
Mech. Dev. 43, 159-173, 1993  
A:Title: A novel cDNA corresponding to transcripts expressed in retina post-mitotic neurogenesis.  
A:Reference number: A56677; MUID:94128599; PMID:8297788

A:Accession: A56677  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-1251 <BID>  
A:Cross-references: GB:S68151; NID:9545153; PIDN:AAD14007.1; PID:94261707  
A:Note: conceptual translation not given

Query Match 9.5%; Score 77.5; DB 2; Length 1251;  
Best Local Similarity 23.5%; Pred. No. 34;  
Matches 38; Conservative 37; Mismatches 64; Indels 23; Gaps 9;

Qy 6 BSKLSVI--RNNDQVLFI---DQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSOPRGM 61  
Db 648 EEKLAQIKEMEDQEVIIQGYQOENRKYKQMKDLQIQNKKEE---QMYKENQCL-MS 702

Qy 62 VTISVKCEKISXLSCKENKIISFKEMNPPDNIKDTKSDIIFQFORSVPGHNMQFSE----- 116  
Db 703 ELIALR-EKVERINQSQIV--RESEPARN--QSFTELISELRRAARKSETKLREIRLUK 757

Qy 117 --SSSYEGYFLACEKERDLFKILKKEDELGRSIMFTVQNE 156  
Db 758 QDKQALELDLQGAQKVERDLAKVQITSTS--SEKSYEFKIMEE 797

RESULT 10  
A81261  
probable periplasmic protein Cj1643 [imported] - Campylobacter jejuni (strain NCTC 11168)  
C:Species: Campylobacter jejuni  
C:Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 03-Jun-2002  
C:Accession: A81261  
R:Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillingworth, N.; et al.



Db 11 GRSDADLVVFLNLTSPFDQNLQOQVLKEIKKQLCEVQHERRC----- 54  
Qy 55 SQRPRGMAVTISVKCEKISXLSKCNKIISFKEMNPPDNIKDTSKDI----- 100  
Db 55 -----GVKFEVSLRSPNSALSPK-LSAPDLKEVKFVDPVLPAYDLLDHLNLIK 103  
Qy 101 -----FFQR---SVP-GHNDKMQFESSYEGYFLACE--KERDLFKLI-----LKKEDEBLG 145  
Db 104 PNOQFYANLISGVPAGKEGKLSICFMGLQKYFLNCRPTKLKRLIRLVTHWYQLCKE-KLG 162  
Qy 146 D 146  
Db 163 D 163

## RESULT 14

I46620  
interleukin-1 alpha precursor - pig  
C:Species: Sus scrofa domestica (domestic pig)  
C>Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 04-Feb-2000  
C:Accession: I46620  
R:Maliszewski, C.  
Nucleic Acids Res. 14, 4282, 1990  
A:Title: Nucleotide sequence of porcine interleukin-1 alpha.  
A:Reference number: I46620  
A:Accession: I46620  
A:Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: mRNA  
A:Residues: 1-270 <MAL>  
A:Cross-references: GB:M86730; NID:g164622; PIDN:AAA73198.1; PID:g164623  
C:Superfamily: interleukin-1  
C:Keywords: lipoprotein; myristylation  
E:1-112/Domain: propeptide #status predicted <PRO>  
E:113-270/Product: interleukin-1 alpha #status predicted <IL1>  
F:82.83/Binding site: myristate (Lys) (covalent) #status predicted

Query Match 9.3%; Score 75.5; DB 2; Length 270;  
Best Local Similarity 22.0%; Pred. No. 8.7;  
Matches 29; Conservative 32; Mismatches 58; Indels 13; Gaps 6;

Qy 8 KLSVIRNLNDQVLFDQGNRPLFEDMTD-----SDCRDNAPRTI-FIISMYKDSQPRGMAY 62  
Db 123 KYNFMRVINHCILNDARNQSIIRDPGQYLMAAVLNLDLDEAVKFDMAAYTSNDDSQLPV 182  
Qy 63 TISVKCEKISXLSKCN--KISFKEM-NPPDNIKDTSKDIIFQSRVPGHNDKMQFESS 119  
Db 183 TLIRIS-ETRLFVSAQNEDEPVLKLPETPKTIKDETSLLFFWEK-----HGNMDYFKSAA 237

Qy 120 YEGVFLACEKER 131

Db 238 HPKLLIATRQEK 249

## RESULT 15

H64245  
hypothetical protein MG414 - Mycoplasma genitalium  
C:Species: Mycoplasma genitalium  
C>Date: 10-Nov-1995 #sequence\_revision 10-Nov-1995 #text\_change 02-Mar-2001  
C:Accession: H64245; G64245  
R:Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.;  
M.; Fuhrmann, J.; Nguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.  
C.A.; Venter, J.C.  
Science 270, 397-403, 1995  
A:Title: The minimal gene complement of Mycoplasma genitalium.  
A:Reference number: A64200; MUID:96026346; PMID:7569993  
A:Accession: H64245  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-1036 <TIGR>  
A:Cross-references: GB:U39727; GB:L43967; NID:g1046127; PID:g1046129; TIGR:MG414  
A:Experimental source: strain G-37  
A:Accession: G64245

A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 'M', 310-1036 <TIG2>  
A:Cross-references: GB:U39727; GB:L43967; NID:g1046127; PID:g1046128; TIGR:MG413  
A:Experimental source: strain G-37  
C:Genetics:  
A:Genetic code: SGC3  
A:Start codon: GTG  
C:Superfamily: hypothetical protein MG413

## Query Match

Best Local Similarity 9.3%; Score 75.5; DB 2; Length 1036;  
Matches 33; Conservative 32; Mismatches 65; Indels 21; Gaps 6;

Qy 14 NLNDQVLFDQGNRPLFED--MTDSDCRDNAPRTIFIISMYKDSQPRGMAYTISVKCEK- 70  
Db 845 SLNDEQLLVKLNITLSEKRLQTTKNVFNKKNKFNILHVENKQFNLFVDVRSKGL 904  
Qy 71 ISXLSKCNKIISFKEMNPPDNIKDTSKDIIFQSRVPGHNDKMQFESSYEGYFLACEK 129  
Db 905 FIGVNDNQVFSISY-----DLKITNQTLIV-DANGFONSIFWFDITS-----EN 950  
Qy 130 ERDLFKLI--LKKEDELGDRSIMFTVQNE 157  
Db 951 QTQLFKALSFYLNKQNNLQFKRVPDPFNLSQD 981

Search completed: August 19, 2004, 13:36:45

Job time : 17 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 19, 2004, 13:31:14 ; Search time 13 Seconds  
(without alignments)  
628.847 Million cell updates/sec

Title: US-09-716-356A-6  
Perfect score: 812  
Sequence: 1 YFGKLESLVIRNLDQVL.....LKKEDELGRSIFMTVQVNE 157

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	ID	Description
1	811	99.9	1 IL18 HUMAN	Q14116 homo sapien
2	659	81.2	1 IL18 HORSE	Q9X897 equus caball
3	654	80.5	1 IL18 BOVIN	Q9TU73 bos taurus
4	637	78.4	1 IL18 PIG	IL19073 sus scrofa
5	613	75.5	1 IL18 CANFA	Q9X8R0 canis famill
6	515	63.4	1 IL18 MOUSE	P70380 mus musculus
7	514.5	63.4	1 IL18 RAT	P97636 rattus norv
8	178.5	22.0	1 IL18 CHICK	Q8QFQ8 gallus gall
9	88	10.8	1 FAT2 DROME	Q9VW71 drosophila
10	81.5	10.0	1 IL1A PIG	P18430 sus scrofa
11	81	10.0	1 IL1A RABIT	P04822 oryctolagus
12	80	9.9	1 DP03 CLOPE	Q8XJX3 clostridium
13	79.5	9.8	1 DNAK_CHLCV	Q824B2 chlamydomophi
14	77.5	9.5	1 MUTL CLOPE	Q8X186 clostridium
15	76.5	9.4	1 IL1A HORSE	Q28385 equus caball
16	75.5	9.3	1 OAGB MOUSE	Q60856 mus musculus
17	75.5	9.3	1 Y414 MYCGE	P47653 mycoplasma
18	75.5	9.3	1 CO3 MOUSE	P01027 mus musculus
19	74.5	9.2	1 EM14 HUMAN	Q13201 homo sapien
20	74	9.1	1 M3X8 MOUSE	Q07174 mus musculus
21	74	9.1	1 M3X8 RAT	Q63562 rattus norv
22	74	9.1	1 MSPI PLAYO	P13828 plasmodium
23	73	9.0	1 IL1A FELCA	Q46613 felis silve
24	73	9.0	1 SYS UREPA	Q9P338 ureaplasma
25	73	9.0	1 YXCX ASTLO	P58151 astasia lon
26	72.5	8.9	1 CO14 ARATH	Q9M5B3 arabidopsis
27	72.5	8.9	1 UVSE CLOPE	Q8XIP3 clostridium
28	71.5	8.8	1 IL1A BOVIN	P08631 bos taurus
29	71.5	8.8	1 M3X8 HUMAN	P41279 homo sapien
30	71.5	8.8	1 RAG2 HUMAN	P55895 homo sapien
31	71	8.7	1 N0NA DROME	Q04047 drosophila
32	70.5	8.7	1 KDSE FUSNN	Q8F8A8 fuscobacteri
33	70.5	8.7	1 IL1A CAPHI	P79161 capra hircu

34	70.5	8.7	644	1 YGM4 YEAST	P53129 saccharomyc
35	70.5	8.7	659	1 DNAK_CHLAB	Q8GH79 chlamydomophi
36	70	8.6	198	1 VS11 ROTRA	P17467 rabbit rota
37	70	8.6	1647	1 SN24 HUMAN	P51532 homo sapien
38	70	8.6	2663	1 CENE HUMAN	Q02224 homo sapien
39	70	8.6	4590	1 FATH HUMAN	Q14517 homo sapien
40	69.5	8.6	268	1 IL1A SHEEP	Q28579 ovis aries
41	69.5	8.6	351	1 RFI TREPA	Q83090 treponema p
42	69.5	8.6	375	1 YVC5 CAEEL	Q18610 caenorhabdi
43	69.5	8.6	582	1 CRTI CAPAN	P80093 capsicum an
44	69.5	8.6	646	1 NOSZ RALSO	Q8XQB8 ralatonia s
45	69.5	8.6	919	1 RPO2_CAPVK	P16716 capripoxvir

#### ALIGNMENTS

RESULT 1  
IL18 HUMAN  
ID IL18 HUMAN STANDARD; PRT; 193 AA.  
AC Q14116; O75599;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Interleukin-18 precursor (IL-18) (interferon-gamma inducing factor)  
DE (IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma).  
GN IL18 OR IGIF.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=livier;  
RX MEDLINE=96247646; PubMed=8666798;  
RA Ushio S., Namba M., Okura T., Hattori K., Nakada Y., Akita K.,  
RA Tanabe F., Konishi K., Micallef M., Fujii M., Torigoe K., Tanimoto T.,  
RA Fukuda S., Ikeda M., Okamura H., Kurimoto M.;  
RA "Cloning of the cDNA for human IFN-gamma-inducing factor, expression  
RT in Escherichia coli, and studies on the biologic activities of the  
RT protein.";  
RT J. Immunol. 156:4274-4279(1996).  
RL [2]  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=urinary bladder;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Straube R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner K.H., Shermen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marushina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;



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OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20012648; PubMed=10547157;
RX Shoda L.K., Zarlenga D.S., Hirano A., Brown W.C.;
RT "Cloning of a cDNA encoding bovine interleukin-18 and analysis of IL-
RT 18 expression in macrophages and its IFN-gamma-inducing activity.";
RL J. Interferon Cytokine Res. 19:1169-1177(1999).
CC -!- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
CC CELLS (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-1 family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
DR EMBL; AF124789; AAF08686.1; -.
DR InterPro; IPR008996; Cytok_IL1 like.
DR InterPro; IPR000975; Interleukin_1.
DR SMART; SM00125; IL1; 1.
KW Cytokine.
FT PROPEP 1 36 BY SIMILARITY.
FT CHAIN 37 193 INTERLEUKIN-18.
SQ SEQUENCE 193 AA; 22347 MW; 65720F199DEA49C4 CRC64;

Query Match 80.5%; Score 654; DB 1; Length 193;
Best Local Similarity 77.1%; Pred. No. 5,4e-54;
Matches 121; Conservative 23; Mismatches 13; Indels 0; Gaps 0;

Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRFLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
Db 37 HFGKLEPKLSIIRNLNDQVLFINQGNQPVFEDMPDSDCSDNAPQTIFIYMYKDSLTRL 96

Qy 61 AVTISVKCEKISXLSCEKNKISFKEMNPPDNKDTKSDIIFQRSVPGHDKNQFESSY 120
Db 97 AVTISVQCKMSTLSCENKISFKEMNPPDNIDNEESDIIFQRSVPGHDKIQFESSLY 156

Qy 121 EGYFLACKEKRDLPKLLKKEDELDGRSMTFTVQNEED 157
Db 157 KGFLACKKENDLPKLLKKEDELDGRSMTFTVQNQN 193

RESULT 4
IL18_PIG
ID IL18_PIG STANDARD; PRT; 192 AA.
AC O19073;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Interleukin-18 precursor (IL-18) (Interferon-gamma inducing factor)
DE (IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma).
GN IL18 OR IGIF.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Foss D.L., Murtaugh M.P.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Penha-Goncalves M.N., Logan N.A., Nicolson L., Onions D.E.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.

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```

RA Muneta Y., Mori Y.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Intestine;
RX MEDLINE=20260994; PubMed=10803849;
RA Fournout S., Dozois C.M., Yerie M., Pinton P., Fairbrother J.M.,
RA Oswald E., Oswald I.P.;
RT "Cloning, chromosomal location, and tissue expression of the gene for
RT pig interleukin-18.";
RL Immunogenetics 51:358-365(2000).
CC -!- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
CC CELLS (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-1 family.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U68701; AAC18415.1; -.
DR EMBL; Y11132; CAA72014.1; -.
DR EMBL; AB010003; BAA24135.1; -.
DR EMBL; AF191088; AAF71200.1; -.
DR GO; GO:0005596; C:extracellular; ISS.
DR GO; GO:0005125; P:cytokine activity; IMP.
DR GO; GO:0001525; P:angiogenesis; ISS.
DR GO; GO:0042033; P:chemokine biosynthesis; ISS.
DR GO; GO:0008625; P:induction of apoptosis via death domain rec. .; IDA.
DR GO; GO:0042035; P:interferon-gamma biosynthesis; IDA.
DR GO; GO:0042104; P:positive regulation of activated T-cell pro. .; ISS.
DR GO; GO:0008284; P:positive regulation of cell proliferation; IDA.
DR InterPro; IPR008996; Cytok_IL1 like.
DR InterPro; IPR000975; Interleukin_1.
DR SMART; SM00125; IL1; 1.
KW Cytokine.
FT PROPEP 1 35 BY SIMILARITY.
FT CHAIN 36 192 INTERLEUKIN-18.
SQ SEQUENCE 192 AA; 22026 MW; 881EA654E221A17A CRC64;

Query Match 78.4%; Score 637; DB 1; Length 192;
Best Local Similarity 75.2%; Pred. No. 2e-52;
Matches 118; Conservative 24; Mismatches 15; Indels 0; Gaps 0;

Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRFLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60
Db 36 YFGKLEPKLSIIRNLNDQVLFINQGNQPVFEDMPDSDCSDNAPQTIFIYMYKDSLTRL 95

Qy 61 AVTISVKCEKISXLSCEKNKISFKEMNPPDNKDTKSDIIFQRSVPGHDKNQFESSY 120
Db 96 AVTISVQCKMSTLSCENKISFKEMNPPDNIDNEESDIIFQRSVPGHDKIQFESSLY 155

Qy 121 EGYFLACKEKRDLPKLLKKEDELDGRSMTFTVQNEED 157
Db 156 KGFLACKKENDLPKLLKKEDELDGRSMTFTVQNQN 192

RESULT 5
IL18_CANFA
ID IL18_CANFA STANDARD; PRT; 193 AA.
AC Q9XSR0;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Interleukin-18 precursor (IL-18) (Interferon-gamma inducing factor)
DE (IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma).
GN IL18 OR IGIF.
OS Canis familiaris (Dog).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=96115;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99309818; PubMed=10380699;
RA Argyle D.J., McGillivray C., Nicolson L., Onions D.E.;
RT "Cloning, sequencing, and characterization of dog interleukin-18.";
RL Immunogenetics 49:541-543(1999).
CC -!- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
CC -!- FUNCTION: AUGMENTS INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
CC CELLS (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-1 family.
CC
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Y11133; CAA72015.1; -.
DR GO; GO:0005576; C:extracellular; TAS.
DR GO; GO:0016506; F:apoptosis activator activity; IEP.
DR GO; GO:0005125; F:cytokine activity; TAS.
DR GO; GO:0005125; F:chemokine biosynthesis; ISS.
DR GO; GO:0008625; P:induction of apoptosis via death domain rec. .; IEP.
DR GO; GO:0042095; P:interferon-gamma biosynthesis; IDA.
DR GO; GO:0042104; P:positive regulation of activated T-cell pro. .; ISS.
DR InterPro; IPR008996; Cytok_IL1_like.
KW Cytokine.
FT PROPEP 1 36 BY SIMILARITY.
FT CHAIN 37 193 INTERLEUKIN-18.
SQ SEQUENCE 193 AA; 22037 MW; 0D973E586F461F25 CRC64;

Query Match 75.5%; Score 613; DB 1; Length 193;
Best Local Similarity 73.7%; Pred. No. 3.5e-50;
Matches 115; Conservative 23; Mismatches 18; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRDNAPRTIFIIISMYKDSQPRGM 60
DB YFGKLEPKLSIRNLNDQVLFVNEGNQVFEVDPDSCTDNAPRTIFIIYMYKDSLRLGL 96
QY 61 AVTISVCKEKSXLSCENKIIISFKEMNPPDNITKDYSDIIFQRSVPGHDKMKQPESSSY 120
DB AVTISVVKYKWTSLCKNKTISFQKMSPPDSINDEGNDIIFQRSVPGHDKIQPESSLY 156
QY 121 EGYFLACKEKRDLFKLILKKEDELGDRSIMFTVQNE 156
DB KGHFLACKKENDLFKLILKDKDENGDKSIMFTVQNK 192

RESULT 6
IL18_MOUSE
ID IL18_MOUSE STANDARD; PRT; 192 AA.
AC P70380;
DT 15-JUL-1998 (Rel. 36, Created)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Interleukin-18 precursor (IL-18) (Interferon-gamma inducing factor)
DE (IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma).
GN IL18 OR IGIF.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=96061009; PubMed=7477296;
RA Okamura H., Teutui H., Komatsu T., Yutsudo M., Hakura A.,

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RA Tanimoto T., Torigoe K., Okura T., Nukada Y., Hattori K.
RA Akita K., Namba M., Tanabe F., Konishi K., Fukuda S., Kurimoto M.;
RT "Cloning of a new cytokine that induces IFN-gamma production by T
RT cells.";
RL Nature 378:88-91(1995).
RN [2]
RP SEQUENCE OF 1-191 FROM N.A.
RC STRAIN=NOD; TISSUE=Pancreas;
RX MEDLINE=97174346; PubMed=9022080;
RA Rothe H., Jenkins N.A., Copeland N.G., Kolb H.;
RT "Active stage of autoimmune diabetes is associated with the
RT expression of a novel cytokine, IGIF, which is located near Idd2.";
RL J. Clin. Invest. 99:469-474(1997).
CC -!- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
CC -!- AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
CC CELLS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-1 family.
CC
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CC -----
DR EMBL; D49949; BAA08705.1; -.
DR EMBL; U66244; AAB49753.1; -.
DR PIR; S60236; S60226.
DR MGI; MGI:107936; IL18.
DR GO; GO:0005576; C:extracellular; ISS.
DR GO; GO:0016506; F:apoptosis activator activity; TAS.
DR GO; GO:0005125; F:cytokine activity; ISS.
DR GO; GO:0001525; P:angiogenesis; ISS.
DR GO; GO:0042033; P:chemokine biosynthesis; ISS.
DR GO; GO:0042253; P:granulocyte macrophage colony-stimulating f. .; ISS.
DR GO; GO:0008625; P:induction of apoptosis via death domain rec. .; TAS.
DR GO; GO:0042095; P:interferon-gamma biosynthesis; IMP.
DR GO; GO:0042231; P:interleukin-13 biosynthesis; TAS.
DR GO; GO:0042104; P:positive regulation of activated T-cell pro. .; ISS.
DR GO; GO:0030155; P:regulation of cell adhesion; ISS.
DR GO; GO:0030431; P:sleep; ISS.
DR InterPro; IPR008996; Cytok_IL1_like.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR SMART; SM00125; IL1; 1.
KW Cytokine.
FT PROPEP 1 35
FT CHAIN 36 192 INTERLEUKIN-18.
FT CONFLICT 183 185 MFT -> IS (IN REF. 2).
SQ SEQUENCE 192 AA; 22135 MW; 8FED938473874D63 CRC64;

Query Match 63.4%; Score 515; DB 1; Length 192;
Best Local Similarity 64.9%; Pred. No. 4.7e-41;
Matches 100; Conservative 27; Mismatches 25; Indels 2; Gaps 2;

QY 2 FGLKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRDNAPRTIFIIISMYKDSQPRGM 61
DB FGLRHCTAVIRNLNDQVLFVDK-RQVPVFDMTDIDQASSEPQTLIIYMYKDSVRGLA 95
QY 62 VTISVCKEKSXLSCENKIIISFKEMNPPDNITKDYSDIIFQRSVPGHDKMKQPESSSYE 121
DB VTLSVKDSKMSLTSLCKNKTISFEEMDPDENDDIQSDLIFFQKRVPGH-NKMEFESSLYE 154
QY 122 GYFLACKEKRDLFKLILKKEDELGDRSIMFTVQNE 155
DB GHFLACQKEDDAFKLILKDKDENGDKSVIMFTLN 189

RESULT 7
IL18_RAT

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ID IL18_RAT STANDARD; PRT; 194 AA.
AC P97636; O88749; P97637;
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Interleukin-18 precursor (IL-18) (Interferon-gamma inducing factor)
DE (IFN-gamma-inducing factor) (Interleukin-1 gamma) (IL-1 gamma).
GN IL18 OR IGIF.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]_TaxID=10116;
RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
RC STRAIN=Sprague-Dawley; TISSUE=Adrenal gland;
RX MEDLINE=97152963; PubMed=8999896;
RA Conti B., Jahng J.W., Tinti C., Son J.H., Joh T.H.;
RT "Induction of interferon-gamma inducing factor in the adrenal
cortex.";
RL J. Biol. Chem. 272:2035-2037(1997).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM BETA).
RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RX MEDLINE=98368130; PubMed=9702748;
RA Culhane A.C., Hall M.D., Rothwell N.J., Luheshi G.N.;
RT "Cloning of rat brain interleukin-18 cDNA.";
RL Mol. Psych. 3:362-366(1998).
CC -!- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
CELLS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Beta;
CC IsoId=P97636-1; Sequence=Displayed;
CC IsoId=P97636-2; Sequences=VSP_002659;
CC -!- SIMILARITY: Belongs to the IL-1 family.
CC
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CC
CC EMBL; U77776; AAC53009.1; -
CC EMBL; U77777; AAC53010.1; -
CC EMBL; AJ222813; CAA11001.1; -
CC GO; GO:0005576; C:extracellular; ISS.
CC GO; GO:0016506; P:apoptosis activator activity; ISS.
CC GO; GO:0005125; P:cytokine activity; ISS.
CC GO; GO:0001525; P:angiogenesis; ISS.
CC GO; GO:0008625; P:induction of apoptosis via death domain rec. .; ISS.
CC GO; GO:0042095; P:interferon-gamma biosynthesis; ISS.
CC GO; GO:0042104; P:positive regulation of activated T-cell pro. .; ISS.
CC GO; GO:0030155; P:regulation of cell adhesion; ISS.
CC GO; GO:0045188; P:regulation of non-REM sleep; TAS.
CC GO; GO:0030431; P:sleep; IDA.
CC InterPro; IPR008996; Cytok_IL1_like.
CC InterPro; IPR000975; Interleukin_1.
CC Pfam; PF00340; IL1; 1.
CC SMART; SM00125; IL1; 1.
CC Cytokine; Alternative splicing.
KW PROPEP 1 36 BY SIMILARITY.
FT CHAIN 37 194 INTERLEUKIN-18.
FT VARSP LIC 121 139 Missing (in isoform Alpha).
FT /FTID=VSP_002659.
FT
FT CONFLICT 4 5 MS -> IP (IN REF. 2).
FT CONFLICT 48 48 I -> M (IN REF. 2).
FT SEQUENCE 194 AA; 22303 MW; E2089AD6F1798450 CRC64;

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Query Match 63.4%; Score 514.5; DB 1; Length 194;
Best Local Similarity 63.2%; Pred. No. 5.3e-41;
Matches 98; Conservative 28; Mismatches 28; Indels 1; Gaps 1;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSCDRDNAPRTIFIFIISMYKDSQPRGM 60
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
37 HFRGLHCTAVIRSINDQVLFVCKENPFVFDMPDIDRTANESQTRLLIYYMKDSEVRGL 96
QY 61 AVTISVCKEKISXLSCEKNKIISFKEMNPPDNKDKTSIIFFQSRVPGHNDKQFESSY 120
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
97 AVTLVKDGRMSTLSCKNKIISFEEMNPPENIDDKSLIPFQKRVPGH-NKMEFESSLY 155

QY 121 EGYFLACEKERDLFKLILKKEDELGDRSMFTVQN 155
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
156 EGHFLACQKEDDAFKLVLRKRDENGKSVMFLLTN 190

RESULT 8
IL18_CHICK STANDARD; PRT; 196 AA.
AC Q8QF08;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Interleukin-18 precursor (IL-18).
GN IL18.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Rothwell L., Buerstedde J.M., Kaiser P.;
RT "Cloning and characterisation of chicken interleukin-18.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
CELLS (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -!- SIMILARITY: Belongs to the IL-1 family.
CC
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CC
CC EMBL; AJ276025; CAC81652.1; -
CC InterPro; IPR008996; Cytok_IL1_like.
KW Cytokine.
FT PROPEP 1 29 POTENTIAL.
FT CHAIN 30 196 INTERLEUKIN-18.
SQ SEQUENCE 196 AA; 22787 MW; 4947DECECCB92414 CRC64;

Query Match 22.0%; Score 178.5; DB 1; Length 196;
Best Local Similarity 34.3%; Pred. No. 1.1e-09;
Matches 60; Conservative 26; Mismatches 68; Indels 21; Gaps 8;

QY 1 YFGKLESKL-----SVIRNLNDQVLFIDQG-NRPLFEDMTDSCDRDNAPRTIFIIISM 51
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
20 YFEELCDAFCKDKTKIKFFRNVSQLLVVRPDLNVAFAEDVTDQEVKSGS-GMYFDIHC 78
QY 52 YKDSQPRG-MAVTISVCKEKISXLSCEKN-----IISFKEMNPPDNKDKTSIIFFQRS 105
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
79 YKTTAPSARMPVAFVSQVEDKSYNMCCKEKGKMWVRFEVGEVPGKDIPG-ESNIIFFKKT 137
QY 106 VPGHNDK-WQFESSSYGYFLACEKERDLFKLILK-----EDELGDRSMFTVQNE 156
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
138 FTSCKSKAFKFEYSLEQGMFLAFEBEDSLRKLILKLPREDEVDETFTKPTVTSHNE 192

```

RESULT 9  
 ID FAT2 DROME STANDARD; PRT: 4705 AA.  
 AC Q9VW71; Q95S51;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Putative fat-like cadherin-related tumor suppressor homolog  
 DE precursor  
 DE precursor  
 GN FAT2 OR CG7749.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OC NCBI Taxid=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Berkeley;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.H.C., Blazek R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abrell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.V., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borkov D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,  
 RA Butris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablo S., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K.J., Dou L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Foeller C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong E., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Laoko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacle J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kimios I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RA "The genome sequence of Drosophila melanogaster.";  
 RN Science 287:2185-2195(2000).  
 RN [2]  
 RP REVISIONS.  
 RX MEDLINE=22426069; PubMed=12537572;  
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,  
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,  
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,  
 RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,  
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,  
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,  
 RA Lewis S.E.;  
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a  
 RT systematic review."  
 RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).  
 RN [3]  
 RP SEQUENCE OF 3837-4705 FROM N.A.

RC STRAIN=Berkeley; TISSUE=Ovary;  
 RX MEDLINE=22426066; PubMed=12537569;  
 RA Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M.,  
 RA George R.A., Guarini H., Kronmiller B., Pacle J.M., Park S., Wan K.H.,  
 RA Rubin G.M., Celniker S.E.;  
 RT "A Drosophila full-length cDNA resource."  
 RL Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002).  
 CC -!- SUBCELLULAR LOCATION: Type 1 membrane protein (potential).  
 CC -!- SIMILARITY: Contains 34 cadherin domains.  
 CC -!- SIMILARITY: Contains 5 EGF-like domains.  
 CC -!- SIMILARITY: Contains 1 laminin G-like domain.  
 CC -----  
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 CC -----  
 DR EMBL; AE003515; AAF49078.2; -  
 DR EMBL; AY060955; AAL28503.1; ALT\_INIT.  
 DR EMBL; AY118666; AAM50035.1; ALT\_INIT.  
 DR HSSP; P15116; INCI.  
 DR FlyBase; FBgn0036930; fat2.  
 DR GO; GO:0005887; C: integral to plasma membrane; ISS.  
 DR GO; GO:0008014; F: calcium-dependent cell adhesion molecule ac. .; ISS.  
 DR GO; GO:0016339; P: calcium-dependent cell-cell adhesion; ISS.  
 DR InterPro; IPR000152; Asx hydroxyl\_S.  
 DR InterPro; IPR002126; Cadherin.  
 DR InterPro; IPR003985; ConA-like lec\_gl.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR InterPro; IPR006209; EGF-like.  
 DR InterPro; IPR006210; IEGF.  
 DR InterPro; IPR001791; Laminin\_G.  
 DR Pfam; PF00028; cadherin; 31.  
 DR Pfam; PF00054; laminin G; 1.  
 DR Pfam; PF00054; laminin G; 1.  
 DR PRINTS; PR00205; CADHERIN.  
 DR SMART; SM00112; CA; 34.  
 DR SMART; SM00181; EGF; 6.  
 DR SMART; SM00282; LamG; 1.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; 1.  
 DR PROSITE; PS00232; CADHERIN\_1; 18.  
 DR PROSITE; PS00268; CADHERIN\_2; 34.  
 DR PROSITE; PS00022; EGF\_1; 5.  
 DR PROSITE; PS01186; EGF\_2; 2.  
 DR PROSITE; PS00026; EGF\_3; 5.  
 DR PROSITE; PS01187; EGF\_Ca; 1.  
 DR PROSITE; PS00025; LAM\_G\_DOMAIN; 1.  
 KW Hypothetical protein; Cell adhesion; Signal; Glycoprotein;  
 KW Transmembrane; Calcium; Calcium-binding; Repeat; EGF-like domain.  
 FT SIGNAL 1 35  
 FT CHAIN 36 4705  
 FT PUTATIVE FAT-LIKE CADHERIN-RELATED TUMOR  
 FT SUPPRESSOR HOMOLOG.  
 FT EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 1648 1668  
 FT DOMAIN 1669 4705  
 FT CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 60 180  
 FT CADHERIN 1.  
 FT DOMAIN 181 288  
 FT CADHERIN 2.  
 FT DOMAIN 289 397  
 FT CADHERIN 3.  
 FT DOMAIN 398 504  
 FT CADHERIN 4.  
 FT DOMAIN 505 610  
 FT CADHERIN 5.  
 FT DOMAIN 611 713  
 FT CADHERIN 6.  
 FT DOMAIN 770 874  
 FT CADHERIN 7.  
 FT DOMAIN 875 977  
 FT CADHERIN 8.  
 FT DOMAIN 978 1085  
 FT CADHERIN 9.  
 FT DOMAIN 1086 1195  
 FT CADHERIN 10.  
 FT DOMAIN 1191 1296  
 FT CADHERIN 11.  
 FT DOMAIN 1297 1402  
 FT CADHERIN 12.  
 FT DOMAIN 1405 1503  
 FT CADHERIN 13.  
 FT DOMAIN 1504 1609  
 FT CADHERIN 14.  
 FT DOMAIN 1610 1714  
 FT CADHERIN 15.

```
FT DOMAIN 1715 1812 CADHERIN 16.
FT DOMAIN 1813 1929 CADHERIN 17.
FT DOMAIN 1930 2030 CADHERIN 18.
FT DOMAIN 2031 2137 CADHERIN 19.
FT DOMAIN 2138 2238 CADHERIN 20.
FT DOMAIN 2239 2338 CADHERIN 21.
FT DOMAIN 2339 2465 CADHERIN 22.
FT DOMAIN 2466 2567 CADHERIN 23.
FT DOMAIN 2568 2670 CADHERIN 24.
FT DOMAIN 2671 2779 CADHERIN 25.
FT DOMAIN 2780 2876 CADHERIN 26.
FT DOMAIN 2877 2983 CADHERIN 27.
FT DOMAIN 2984 3088 CADHERIN 28.
FT DOMAIN 3089 3185 CADHERIN 29.
FT DOMAIN 3186 3289 CADHERIN 30.
FT DOMAIN 3290 3394 CADHERIN 31.
FT DOMAIN 3395 3499 CADHERIN 32.
FT DOMAIN 3500 3604 CADHERIN 33.
FT DOMAIN 3605 3712 CADHERIN 34.
FT DOMAIN 3713 3819 EGF-LIKE 1.
FT DOMAIN 3820 3919 EGF-LIKE 2.
FT DOMAIN 3920 4019 LAMININ G-LIKE.
FT DOMAIN 4020 4121 EGF-LIKE 3.
FT DOMAIN 4122 4229 EGF-LIKE 4.
FT DOMAIN 4230 4329 EGF-LIKE 5.
FT DISULFID 3823 3835 POTENTIAL.
FT DISULFID 3836 3867 POTENTIAL.
FT DISULFID 3868 3878 POTENTIAL.
FT DISULFID 3879 3896 POTENTIAL.
FT DISULFID 3897 3907 POTENTIAL.
FT DISULFID 3908 3918 POTENTIAL.
FT DISULFID 4133 4144 POTENTIAL.
FT DISULFID 4145 4154 POTENTIAL.
FT DISULFID 4155 4165 POTENTIAL.
FT DISULFID 4166 4183 POTENTIAL.
FT DISULFID 4184 4193 POTENTIAL.
FT DISULFID 4194 4204 POTENTIAL.
FT DISULFID 4205 4258 POTENTIAL.
FT DISULFID 4259 4267 POTENTIAL.
FT DISULFID 4268 4278 POTENTIAL.
FT CARBOHYD 65 65 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 156 156 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 364 364 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 779 779 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 843 843 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 923 923 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1106 1106 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1198 1198 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1312 1312 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1439 1439 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1473 1473 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1511 1511 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 362 362 G -> E (IN REF. 3; AAL28503).
SQ SEQUENCE 4705 AA; 524564 MW; 6D387A489D2C33DE CRC64;

Query Match 10.8%; Score 88; DB 1; Length 4705;
Best Local Similarity 23.6%; Pred. No. 13;
Matches 38; Conservative 25; Mismatches 56; Indels 42; Gaps 7;

Qy 32 DMTDSDCRDNPRTTIFISMY-----KDSQPRGMATVISVKCKISKLSKCNKIISF--KE 85
Db 2124 DISVLVDVNDNCP--LFVNNPYVATVISDDPKG---TIIMQVKAIDLDIAENGVEVYELKK 2178
Qy 86 MNPPDNIDKTSKDIIFQFQSVPHDKNQFESSSYEGYFLACEKERDL----- 133
Db 2179 NGNELFKLDRKSGELSIKHQVHGRNRYELTVAAAYDGAITPCSSAPLQVKVIDRMPVF 2238
Qy 134 ---FKLILKKED-----ELGDRSIMFTVQNE 156
Db 2239 EKQFTVSKEDVEMYSALSVSIEAESPLG-RSLIYITISSE 2278

RESULT 10
```

```
IL1A_PIG
ID IL1A_PIG STANDARD; PRT; 270 AA.
AC P18430;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Interleukin-1 alpha precursor (IL-1 alpha).
GN IL1A.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=90332454; PubMed=2377484;
RA Maliszewski C.R., Renshaw B.R., Schoenborn M.A., Urban J.F.,
RA Baker P.E.;
RT "Porcine IL-1 alpha cDNA nucleotide sequence.";
RL Nucleic Acids Res. 18:4282-4282(1990).
RN [2]
RP SEQUENCE FROM N.A.
RA Huebner M.J., Scamurra R.W., Murtaugh M.P., Molitor T.W.;
RL Submitted (XXI-1992) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
CC THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
CC MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
CC IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
CC -!- SUBUNIT: Monomer.
CC -!- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
CC AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
CC -!- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
CC PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
CC OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
CC SECRETORY PROTEINS.
CC -!- SIMILARITY: Belongs to the IL-1 family.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC
CC EMBL; X52731; CAA36945.1; -.
CC EMBL; M86730; AAA73198.1; -.
CC PIR; I46620; I46620.
CC PIR; S10532; S10532.
CC HSSP; P01593; 11TA.
CC InterPro; IPR008996; Cytok_IL1_like.
CC InterPro; IPR003502; IL1_propep.
CC InterPro; IPR000975; Interleukin_1.
CC Pfam; PF00340; IL1; 1.
CC Pfam; PF02394; IL1_propep; 1.
CC SMART; SM00125; IL1; 1.
CC PROSITE; PS00253; INTERLEUKIN_1; 1.
KW Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.
FT PROPEP 1 112
FT CHAIN 113 270 INTERLEUKIN-1 ALPHA.
FT CARBOHYD 102 102 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 141 141 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 89 89 N -> I (IN REF. 2).
FT CONFLICT 242 242 F -> L (IN REF. 2).
FT CONFLICT 255 255 P -> R (IN REF. 2).
SQ SEQUENCE 270 AA; 5677BF2B0EF63839 CRC64;

Query Match 10.0%; Score 81.5; DB 1; Length 270;
Best Local Similarity 22.7%; Pred. No. 1.7;
Matches 30; Conservative 32; Mismatches 57; Indels 13; Gaps 6;
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QY 8 KLSVIRNLNDVLFIDQGNRPLFEDMTD-----SDCRDNAPRTI-FIISMYKDSQPRGMAY 62
Db 123 KYNFMRVNHQICILNDRARQSGIIRDPSCQYLMAAVLNNLDRAVDFDMAAYTSNDDSQLPV 182
QY 63 TISVKCEKISXLSNEN--KIISFKEM-NPPDNKIDTKSDIIFFORSVPGHNDKMQFESSS 119
Db 183 TLRIS-ETRLFSQAQNEDEPVLKLPETPKTKIDTSLLFFWEK-----HGMNDFKSA 237
QY 120 YEGYFLACEKER 131
Db 238 HPKLFIAATROEK 249

RESULT 11
IL1A_RABIT
ID IL1A_RABIT STANDARD; PRT; 267 AA.
AC P04822;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Interleukin-1 alpha precursor (IL-1 alpha).
GN IL1A.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85297782; PubMed=2994016;
RA Furutani Y., Notake M., Yamayoshi M., Yamagishi J., Nomura H.,
RA Ohue M., Furuta R., Fukui T., Yamada M., Nakamura S.;
RT "Cloning and characterization of the cDNAs for human and rabbit
interleukin-1 precursor."
RL Nucleic Acids Res. 13:5869-5882(1985).
CC -!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
CC THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
CC MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
CC IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
CC -!- SUBUNIT: Monomer.
CC -!- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
CC AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
CC -!- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
CC PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
CC OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
CC SECRETORY PROTEINS.
CC -!- SIMILARITY: Belongs to the IL-1 family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X02852; CAA26605.1; -.
CC HSSP; P01583; 1ITA.
CC InterPro; IPR008996; Cytok IL1 like.
CC InterPro; IPR003502; IL1_propep.
CC InterPro; IPR000975; Interleukin_1.
CC Pfam; PF00340; IL1; 1.
CC Pfam; PF02394; IL1_propep; 1.
CC SMART; SM00125; IL1; 1.
CC PROSITE; PS00253; INTERLEUKIN_1; 1.
CC Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.
CC PROPEP 1 112
CC CHAIN 113 267 INTERLEUKIN-1 ALPHA.
CC CARBOHYD 64 64 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC SEQUENCE 267 AA; 30375 MW; 6D20533FD1FA4822 CRC64;
SQ

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Query Match 10.0%; Score 81; DB 1; Length 267;
Best Local Similarity 25.2%; Pred. No. 1.9;
Matches 32; Conservative 27; Mismatches 56; Indels 12; Gaps 5;

QY 12 IRNLNDVLFIDQGNRPLFEDMTDSDCRDNAPRTI-----FIISMYKDSQPRGMAYTISV 66
Db 127 LRIIKQFTLNDALNQSLVRDTSQYLRAPLQNLGDAVKFDMGVYMTSESDILPVTURI 186
QY 67 KCEKISXLSNEN--KIISFKEM-NPPDNKIDTKSDIIFFORSVPGHNDKMQFESSYEGY 123
Db 187 SQTPL-FVSAQNEDEPVLKLPETPKTIITDSBILFFWET---QGNKNFYKSAANPOL 242
QY 124 FLACEKE 130
Db 243 FIATKPE 249

RESULT 12
DPO3_CLOPE
ID DPO3_CLOPE STANDARD; PRT; 1449 AA.
AC Q8XJR3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE DNA polymerase III polC-type (EC 2.7.7.7) (PolIII).
GN POLC OR CPEL691.
OS Clostridium perfringens.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1502;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=13 / Type A;
RX MEDLINE=21664373; PubMed=11792842;
RA Shimizu T., Ohtani K., Hirakawa H., Ohehima K., Yamashita A.,
RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
RT "Complete genome sequence of Clostridium perfringens, an anaerobic
flesh-eater."
RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
CC -!- FUNCTION: Required for replicative DNA synthesis. This DNA
CC polymerase also exhibits 3' to 5' exonuclease activity (By
CC similarity).
CC -!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
CC + {DNA} (N).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the DNA polymerase type-C family. PolC
CC subfamily.
CC
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CC
CC EMBL; AP003191; BAB81397.1; -.
CC HAMAP; MF 00356; -.
CC InterPro; IPR006054; DnaQ.
CC InterPro; IPR006055; Exonuclease.
CC InterPro; IPR004013; PNP_C.
CC InterPro; IPR003141; PNP_N.
CC InterPro; IPR006308; PolC_gram_pos.
CC Pfam; PF00929; Exonuclease; 1.
CC Pfam; PF02811; PNP_C; 1.
CC Pfam; PF02231; PNP_N; 1.
CC SMART; SM00479; EXOIII; 1.
CC SMART; SM00481; POLIIIAC; 1.
CC TIGRFAMs; TIGR01405; polC_gram_pos; 1.
CC Transferrase; DNA-directed DNA polymerase; DNA replication; Hydrolase;
CC Nuclease; Exonuclease; Complete proteome.
KW

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OM protein - protein search, using sw model

Run on: August 19, 2004, 13:32:15 ; Search time 39 Seconds  
(without alignments)  
1270.163 Million cell updates/sec

Title: US-09-716-356A-6  
Perfect score: 812  
Sequence: 1 YFGKLESKSLVIRNLNDQVL.....LKKEDELGRSIMFTVQNEED 157

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues  
Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_25:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phase:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match	Length	DB	ID	Description
1	798	98.3	193	4	Q96KJ8	Q96KJ8	homo sapien
2	792	97.5	193	6	Q9BG15	Q9BG15	macaca mula
3	654	80.5	178	6	Q9MZL8	Q9MZL8	bos taurus
4	648	79.8	193	6	Q9GL09	Q9GL09	ovis aries
5	634	78.1	192	6	Q9SM33	Q9SM33	felis silve
6	633	78.0	192	6	Q8E5B8	Q8E5B8	felis silve
7	626	77.1	192	6	Q9N1P7	Q9N1P7	bus scrofa
8	536.5	66.1	195	11	Q8QY07	Q8QY07	meriones un
9	515	63.4	189	11	Q8QSS8	Q8QSS8	mus musculus
10	441	54.3	196	11	Q91Z66	Q91Z66	sigmodon hi
11	313	38.5	84	6	Q95LE7	Q95LE7	canis famil
12	204	25.1	45	4	Q9NQ49	Q9NQ49	homo sapien
13	193	23.8	211	13	Q98SQ1	Q98SQ1	anas platyr
14	184.5	22.7	198	13	Q8AV26	Q8AV26	meleagris g
15	182.5	22.5	198	13	Q918D2	Q918D2	gallus gall
16	86.5	10.7	376	11	Q8K4E7	Q8K4E7	mus musculus

17	86.5	10.7	376	11	Q8K4E6	Q8K4E6	mus musculus
18	85	10.5	252	11	Q8JZN4	Q8JZN4	mus musculus
19	85	10.5	381	3	Q43031	Q43031	schizosacch
20	84.5	10.4	376	11	Q8K4E8	Q8K4E8	mus musculus
21	83.5	10.3	454	6	Q8HZU7	Q8HZU7	tonatia sau
22	83.5	10.3	454	6	Q8HZU6	Q8HZU6	tonatia sau
23	83.5	10.3	454	6	Q8HZU5	Q8HZU5	tonatia sau
24	83	10.2	376	11	Q8JZN0	Q8JZN0	mus musculus
25	82.5	10.2	268	6	Q8E5X7	Q8E5X7	lama glama
26	82	10.1	263	3	Q74316	Q74316	schizosacch
27	82	10.1	1534	5	Q8MPV7	Q8MPV7	caenorhabdi
28	81.5	10.0	599	5	Q8I2G6	Q8I2G6	plasmodium
29	81.5	10.0	617	5	Q25986	Q25986	plasmodium
30	81.5	10.0	1049	2	Q93KF0	Q93KF0	caidicellul
31	80.5	9.9	825	5	Q8IC17	Q8IC17	plasmodium
32	80.5	9.9	866	16	Q84500	Q84500	chlamydia t
33	79.5	9.8	595	10	Q9SDM4	Q9SDM4	dunaliella
34	79.5	9.8	1044	3	Q94173	Q94173	pneumocysti
35	79	9.7	452	16	Q25249	Q25249	helicobacte
36	79	9.7	10578	5	Q8ISF5	Q8ISF5	caenorhabdi
37	79	9.7	18519	5	Q8ISF6	Q8ISF6	caenorhabdi
38	79	9.7	18534	5	Q8ISF7	Q8ISF7	caenorhabdi
39	78.5	9.7	204	2	Q9ZNU7	Q9ZNU7	clostridium
40	78.5	9.7	1061	16	Q8DU02	Q8DU02	streptococc
41	78	9.6	261	16	Q8CU21	Q8CU21	staphylococ
42	78	9.6	277	16	Q8DUA4	Q8DUA4	staphylococ
43	78	9.6	473	5	Q16673	Q16673	caenorhabdi
44	78	9.6	2578	5	Q8IJP9	Q8IJP9	plasmodium
45	77.5	9.5	454	6	Q8HZU4	Q8HZU4	tonatia bid

ALIGNMENTS

RESULT 1  
Q96KJ8  
ID Q96KJ8 PRELIMINARY; PRT; 193 AA.  
AC Q96KJ8;  
DT 01-DEC-2001 (Tremblrel. 19, Created)  
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)  
DE Interleukin 18.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]\_TaxID=9606;  
RP SEQUENCE FROM N.A.  
RA Ying P., Jianxin L.;  
RT "Cloning of Mutant Human Interleukin 18 cDNA."  
RL Submitted (MAY-2001) to the EMBL/GenBank/DBSJ databases.  
DR EMBL; AF380360; AAKS7024.1;  
DR GO; GO:0005576; C:extracellular; IEA.  
DR GO; GO:0005149; F:interleukin-1 receptor binding; IEA.  
DR GO; GO:0006955; P:immune response; IEA.  
DR InterPro; IPR008996; Cytok IL1 like.  
DR InterPro; IPR000975; Interleukin\_1.  
DR SMART; SM00125; IL1; 1.  
SQ SEQUENCE 193 AA; 22323 MW; 2E500205D1B7E5F7 CRC64;  
Query Match 98.3%; Score 798; DB 4; Length 193;  
Best Local Similarity 97.5%; Pred. No. 2.7e-71;  
Matches 153; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
QY 1 YFGKLESKSLVIRNLNDQVLFDQGNRFLFEDMTSDCRDNAPRTIFITSMYKDSQPRGM 60  
DB 1 YFGKLESKSLVIRNLNDQVLFDQGNRFLFEDMTSDCRDNAPRTIFITSMYKDSQPRGM 96  
QY 61 AVTISVKCEKSLSCENKIISFKEMNPDPNIDKTSIIIFQSVPGHDNKKQFESSY 120  
DB 97 AVTISVKCEKSLSCENKIISFKEMNPDPNIDKTSIIIFQSVPGHDNKKQFESSY 156  
QY 121 EGYFLACEKERDLFKLILKKEDELGRSIMPFTVQNEED 157

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Db 157 EGYFLTCERDLFKLILKKDELDGDRSIMFTVQNE 193
|||||
RESULT 2
Q9BG15 PRELIMINARY; PRT; 193 AA.
ID Q9BG15
AC Q9BG15
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Interleukin-18.
GN IL18.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21229850; PubMed=11331040;
RA Giavedoni L.D., Imhoof J.D., Farodi L.M., Velasquillo C.M.,
RA Hodara V.L.;
RT "Expression of the Interleukin-18 Gene from Rhesus Macaque by the
RT Simian Immunodeficiency Virus Does Not Result In Increased Viral
RT Replication."
RL J. Interferon Cytokine Res. 21:173-180(2001).
DR EMBL; AF303732; AAK13416.1; -.
DR InterPro; IPR008996; Cytok IL1 like.
SQ SEQUENCE 193 AA; 22325 MW; B2BD29C03BB0B5E CRC64;

Query Match 97.5%; Score 792; DB 6; Length 193;
Best Local Similarity 95.5%; Pred. No. 1.1e-70;
Matches 150; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYSQSPGRGM 60
|||||
Db 37 YFGKLESKLSIIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIINYSQSPGRGM 96
|||||
Qy 61 AVTISVCKEKSIXLSCENKIISFKEMNPPDNKOTKSDIIFQSRVPGHDNKMOPESSY 120
|||||
Db 97 AVAISVCKEKSIXLSCENKIISFKEMNPPDNKOTKSDIIFQSRVPGHDNKMOPESSY 156
|||||
Qy 121 EGYFLACEKERDLFKLILKKDELDGDRSIMFTVQNE 157
|||||
Db 157 EGYFLACEKERDLFKLILKKDELDGDRSIMFTVQNE 193
|||||

RESULT 3
Q9MZL8 PRELIMINARY; PRT; 178 AA.
ID Q9MZL8
AC Q9MZL8
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Interleukin-18 (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney, Liver, and Blood;
RA Olsen S.C., Lee I.K., Mwangi S.M., Kehrli M., Bolin C.A.;
RT "Cloning of bovine interleukin-18, expression in Escherichia coli, and
RT characterization of the biologic activities of the recombinant
RT cytokine."
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF173175; AAF89833.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005149; F:interleukin-1 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
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DR InterPro; IPR008996; Cytok IL1 like.
DR InterPro; IPR000975; Interleukin_1.
DR SMART; SM00125; IL1; 1.
FT NON_TER 1
FT NON_TER 178
SQ SEQUENCE 178 AA; 20631 MW; 816DGB2B88ACB497 CRC64;

Query Match 80.5%; Score 654; DB 6; Length 178;
Best Local Similarity 77.1%; Pred. No. 4.9e-57;
Matches 121; Conservative 23; Mismatches 13; Indels 0; Gaps 0;

Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYSQSPGRGM 60
|||||
Db 22 HFGKLEPKLSIIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIINYSQSLTRGL 81
|||||
Qy 61 AVTISVCKEKSIXLSCENKIISFKEMNPPDNKOTKSDIIFQSRVPGHDNKMOPESSY 120
|||||
Db 82 AVTISVCKEKSIXLSCENKIISFKEMNPPDNKOTKSDIIFQSRVPGHDNKMOPESSY 141
|||||
Qy 121 EGYFLACEKERDLFKLILKKDELDGDRSIMFTVQNE 157
|||||
Db 142 KGYFLACKENDLFKLILKKQDDNRDKSVMTVQNN 178
|||||

RESULT 4
Q9GL09 PRELIMINARY; PRT; 193 AA.
ID Q9GL09
AC Q9GL09
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Interleukin-18 (IGIF).
GN IL-18.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RA Bailey S.L., Gossner A., Dalziel R., Hopkins J.;
RT "Cloning of Ovine Interleukin 18 cDNA."
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ401033; CAC09326.2; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005149; F:interleukin-1 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR008996; Cytok IL1 like.
DR InterPro; IPR000975; Interleukin_1.
DR SMART; SM00125; IL1; 1.
SQ SEQUENCE 193 AA; 22166 MW; CCD0A329062EF18C CRC64;

Query Match 79.8%; Score 648; DB 6; Length 193;
Best Local Similarity 77.7%; Pred. No. 2.1e-56;
Matches 122; Conservative 20; Mismatches 15; Indels 0; Gaps 0;

Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYSQSPGRGM 60
|||||
Db 37 HFGKLEPKLSIIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIINYSQSLTRGL 96
|||||
Qy 61 AVTISVCKEKSIXLSCENKIISFKEMNPPDNKOTKSDIIFQSRVPGHDNKMOPESSY 120
|||||
Db 97 AVTISVCKEKSIXLSCENKIISFKEMNPPDNKOTKSDIIFQSRVPGHDNKMOPESSY 156
|||||
Qy 121 EGYFLACEKERDLFKLILKKDELDGDRSIMFTVQNE 157
|||||
Db 157 KGYFLACKENDLFKLILKKQDDNRDKSVMTVQNN 193
|||||

RESULT 5
Q9SM33 PRELIMINARY; PRT; 192 AA.
ID Q9SM33
AC Q9SM33
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DT 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
 DE Interferon-gamma inducing factor.  
 GN IGIF.  
 OS Felis silvestris catus (Cat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
 OX NCBI\_TaxID=9685;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Hanlon L., McGillivray C.P., Argyle D.J.A., Nicolson L., Onions D.E.;  
 RT "Nucleotide sequence of feline IGIF cDNA (provisional).";  
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; Y13923; CAC42918.1; -.  
 DR InterPro; IPR008996; Cytok\_IL1\_like.  
 SQ SEQUENCE 192 AA; 22068 MW; 5878C3DAC7A43358 CRC64;  
  
 Query Match 78.1%; Score 634; DB 6; Length 192;  
 Best Local Similarity 76.4%; Pred. No. 5.1e-55;  
 Matches 120; Conservative 21; Mismatches 16; Indels 0; Gaps 0;  
  
 QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCEDNAPRTIFIISMVKDSQPRGM 60  
 DB 36 YFGKLEHLKLSIRNLNDQVLFIDQGNRPLFEDMTSDCEDNAPRTIFIISMVKDSLTRLGL 95  
  
 QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNKDTKSDIIFQRSVPVGHDKMKQFESSY 120  
 DB 96 AVTISVNTKMTLSCEKNIISFKEMSPESINDEGNDIIFQRSVPVGHDKMKQFESSLY 155  
  
 QY 121 EGYFLACEKERDLFKLILKKEDELGRSIFMTVQNE 157  
 DB 156 KGYFLACEKERDLFKLILKKEDELGRSIFMTVQNK 192  
  
 RESULT 6  
 Q865B8  
 ID Q865B8 PRELIMINARY; PRT; 192 AA.  
 AC Q865B8;  
 DT 01-JUN-2003 (TREMBlrel. 24, Created)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
 DE Interferon gamma inducing factor precursor.  
 GN FIL-18.  
 OS Felis silvestris catus (Cat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
 OX NCBI\_TaxID=9685;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Kuwahara C., Kawakami K., Kishi M., Mochizuki M.;  
 RT "Feline interleukin-18";  
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB056857; BAC65243.1; -.  
 DR InterPro; IPR008996; Cytok\_IL1\_like.  
 KW SIGNAL.  
 FT SIGNAL.  
 SQ SEQUENCE 192 AA; 22071 MW; 204F32D131588513 CRC64;  
  
 Query Match 78.0%; Score 633; DB 6; Length 192;  
 Best Local Similarity 76.9%; Pred. No. 6.4e-55;  
 Matches 120; Conservative 20; Mismatches 16; Indels 0; Gaps 0;  
  
 QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCEDNAPRTIFIISMVKDSQPRGM 60  
 DB 36 YFGKLEHLKLSIRNLNDQVLFIDQGNRPLFEDMTSDCEDNAPRTIFIISMVKDSLTRLGL 95  
  
 QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNKDTKSDIIFQRSVPVGHDKMKQFESSY 120  
 DB 96 AVTISVNTKMTLSCEKNIISFKEMSPESINDEGNDIIFQRSVPVGHDKMKQFESSLY 155  
  
 QY 121 EGYFLACEKERDLFKLILKKEDELGRSIFMTVQNE 156  
 DB 156 KGYFLACEKERDLFKLILKKEDELGRSIFMTVQNK 192

DB 156 KGYFLACEKERDLFKLILKKEDELGRSIFMTVQNK 191  
  
 RESULT 7  
 Q9N1P7  
 ID Q9N1P7 PRELIMINARY; PRT; 192 AA.  
 AC Q9N1P7;  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
 DE Interleukin-18.  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 OX NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lung;  
 RX MEDLINE=20356335; PubMed=10901174;  
 RA Oem J.K., Song H.J., Kang S.W., Jeong W.S.;  
 RT "Cloning, sequencing, and expression of porcine interleukin-18 in  
 Escherichia coli";  
 RL Mol. Cells 10:343-347(2000).  
 DR EMBL; AF176949; AAF35169.1; -.  
 DR GO; GO:0005576; C:extracellular; IEA.  
 DR GO; GO:0005149; F:interleukin-1 receptor binding; IEA.  
 DR GO; GO:0006985; P:immune response; IEA.  
 DR InterPro; IPR008996; Cytok\_IL1\_like.  
 DR InterPro; IPR000975; Interleukin\_1.  
 DR SMART; SM00125; IL1; 1.  
 SQ SEQUENCE 192 AA; 21969 MW; A51EB7A4E221A16D CRC64;  
  
 Query Match 77.1%; Score 626; DB 6; Length 192;  
 Best Local Similarity 73.9%; Pred. No. 3.2e-54;  
 Matches 116; Conservative 25; Mismatches 16; Indels 0; Gaps 0;  
  
 QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCEDNAPRTIFIISMVKDSQPRGM 60  
 DB 36 YFGKLEPKLSIRNLNDQVLFIDQGNRPLFEDMTSDCEDNAPRTIFIISMVKDSLTRLGL 95  
  
 QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNKDTKSDIIFQRSVPVGHDKMKQFESSY 120  
 DB 96 AVTISVQCKKMTLSCKNKTLTKFEMSPDNIDDEGNDIIFQRSVPVGHDKMKQFESSLY 155  
  
 QY 121 EGYFLACEKERDLFKLILKKEDELGRSIFMTVQNE 157  
 DB 156 KGYFLACEKERDLFKLILKKEDELGRSIFMTVQSKN 192  
  
 RESULT 8  
 Q80Y07  
 ID Q80Y07 PRELIMINARY; PRT; 195 AA.  
 AC Q80Y07;  
 DT 01-JUN-2003 (TREMBlrel. 24, Created)  
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
 DE Interleukin 18.  
 GN IL18.  
 OS Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;  
 OC Meriones.  
 OX NCBI\_TaxID=10047;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Peritoneum;  
 RX MEDLINE=22593022; PubMed=12706898;  
 RA Gaucher D., Chadee K.;  
 RT "Gerbil interleukin-18 and caspase-1: cloning, expression and  
 characterization";  
 RL Gene 307:159-166(2003).  
 DR EMBL; AY095932; AAM34434.1; -.  
 DR InterPro; IPR008996; Cytok\_IL1\_like.

```
SQ SEQUENCE 195 AA; 22172 MW; C6P815317953154D CRC64;
Query Match 66.1%; Score 536.5; DB 11; Length 195;
Best Local Similarity 65.8%; Pred. No. 2.5e-45;
Matches 100; Conservative 29; Mismatches 22; Indels 1; Gaps 1;

QY 2 FGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGMA 61
DB 39 FGRLSSTAVIRNINEQVLFVDGRKQPFEDMTDAEQANGQTLLIIMYKDTFARGLA 98
QY 62 VTISVKCEKISXLSCKENKIIISFKENPPDNIKOTKSDIIFQFORSVPGHDKNQPFSSSYE 121
DB 99 VTLISKDTTATLSCKNKIIISFEENPPENIDDTESDLIFQKRVPGH-NKMQFESSLYK 157

QY 122 GYFLACEKERDLFKLILKKEDELGDRSIMFTVN 153
DB 158 GHFLACQKEEDAFKILKKKQDNGDKSVNFTV 189

RESULT 9
Q80SS8 PRELIMINARY; PRT; 189 AA.
AC Q80SS8;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Interleukin 18.
GN IL18.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B10.S/DvTe, and SJL/J; TISSUE=Spleen;
RA Gao J., Teuscher C.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY157834; AAC21309.1; -.
DR EMBL; AY157835; AAC21310.1; -.
DR InterPro; IPR008996; Cytok_IL1 like.
SQ SEQUENCE 189 AA; 21862 MW; E8P95EC01864665 CRC64;

Query Match 63.4%; Score 515; DB 11; Length 189;
Best Local Similarity 64.9%; Pred. No. 3.2e-43;
Matches 100; Conservative 27; Mismatches 25; Indels 2; Gaps 2;

QY 2 FGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGMA 61
DB 34 FGRLHCTAVIRNINDQVLFVDK-RQPFEDMTDIDQASSEFQTLIIIMYKDSVIRGLA 92
QY 62 VTISVKCEKISXLSCKENKIIISFKENPPDNIKOTKSDIIFQFORSVPGHDKNQPFSSSYE 121
DB 93 VTLISKDKMSTLSCKNKIIISFEENPPENIDDIQSDLIIFQKRVPGH-NKMEFESSLYE 151

QY 122 GYFLACEKERDLFKLILKKEDELGDRSIMFTVN 155
DB 152 GHFLACQKEEDAFKILKKKQDNGDKSVNFTLN 185

RESULT 10
Q91Z66 PRELIMINARY; PRT; 196 AA.
AC Q91Z66;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Interleukin 18.
GN IL18.
OS Sigmodon hispidus (Hispid cotton rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Sigmodon.
OX NCBI_TaxID=42415;

[1]
RN SEQUENCE FROM N.A.
RP Blanco J.C., Platenava L.M., Prince G.A.;
RT "Sigmodon hispidus cytokines, chemokines and interferons.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY059406; AAL26703.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005149; F:interleukin-1 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR008996; Cytok_IL1 like.
DR InterPro; IPR000975; Interleukin_1.
DR SMART; SM00125; IL1; 1.
SQ SEQUENCE 196 AA; 22545 MW; E27C5BDC397F951C CRC64;

Query Match 54.3%; Score 441; DB 11; Length 196;
Best Local Similarity 59.4%; Pred. No. 7.5e-36;
Matches 92; Conservative 24; Mismatches 37; Indels 2; Gaps 2;

QY 2 FGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVK-DSQPRGM 60
DB 39 FFKESSTAVIRNNNDYVLFIDREKSPVFEDMPDADQKANAQTRLLIIMYKDTFNPGL 98
QY 61 AVTISVKCEKISXLSCKENKIIISFKENPPDNIKOTKSDIIFQFORSVPGHDKNQPFSSSY 120
DB 99 PVTLSVRDRTWRTLSCKNQIIISFEEMPPLIDGTGKSDLIIFQRAVPGH-NKMKFESSLIH 157

QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVN 155
DB 158 EGHLACERDGSFKLILKKKDNWNTSIIFTVTN 192

RESULT 11
Q95LE7 PRELIMINARY; PRT; 84 AA.
AC Q95LE7;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE IL-18 (Fragment).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Chamizo C., Rubio J.M., Moreno J., Alvar J.;
RT "Semi-quantification of canine cytokine expression by one tube RT-PCR.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF327900; AAL26920.1; -.
DR InterPro; IPR008996; Cytok_IL1 like.
FT NON_TER 1 84
FT TER 84 84
SQ SEQUENCE 84 AA; 9568 MW; 19BD9E27F336774B CRC64;

Query Match 38.5%; Score 313; DB 6; Length 84;
Best Local Similarity 74.7%; Pred. No. 1.5e-23;
Matches 59; Conservative 10; Mismatches 10; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60
DB 5 YFGKLEPKLSIIRNLNDQVLFVNEGNEQVFDMPDSDCTDNAPHTIFIIMYKDSLTRGL 64
QY 61 AVTISVKCEKISXLSCKENK 79
DB 65 AVTISVKYKTMSTLSCKNK 83

RESULT 12
Q9NQ49 PRELIMINARY; PRT; 45 AA.
AC Q9NQ49;
ID Q9NQ49
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DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Interleukin-18 (Fragment).
GN IL-18.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Fathan A.J., Pravica V., Hutchinson I.V.;
RT "Identification of Human Interleukin-18 gene polymorphisms.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AJ295724; CAC01436.1; -.
DR InterPro; IPR008996; Cytok_IL1_like.
FT NON_TER 1
FT NON_TER 45
FT NON_TER 45
SQ SEQUENCE 45 AA; 5266 MW; DF3A626507E3D61A CRC64;

Query Match 25.1%; Score 204; DB 4; Length 45;
Best Local Similarity 100.0%; Pred. No. 4.7e-13;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCR 39
DB 7 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCR 45

RESULT 13
Q98SQ1 PRELIMINARY; PRT; 211 AA.
AC Q98SQ1;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Interleukin-18 (Fragment).
GN IL-18.
OS Anas platyrhynchos (Domestic duck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauromia; Aves; Neognathae; Anseriformes; Anatidae; Anas.
OX NCBI_TaxID=8839;
RN [1]
RP SEQUENCE FROM N.A.
RA Chan W.-S., Warr G.W., Middleton D.L., Lundquist M.L., Higgins D.A.;
RT "Anas platyrhynchos T-cell antigens, IL-18 gene.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF336122; AAK26322.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005149; F:interleukin-1 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR008996; Cytok_IL1_like.
DR InterPro; IPR000375; Interleukin_1.
DR SMART; SM00125; IL1; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 211 AA; 24541 MW; CA6FC63538211B2B CRC64;

Query Match 23.8%; Score 193; DB 13; Length 211;
Best Local Similarity 36.5%; Pred. No. 3.3e-11;
Matches 61; Conservative 29; Mismatches 63; Indels 14; Gaps 9;

QY 2 FGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRNAPRTIFIISMVKDSQP-RG 59
DB 43 FSKETLHRLFNVSQVLLVVRPDLNMAAFEDVTDQEMKSGGMN-FCMHCYKTTTPSAG 101

QY 60 MAVTISVKCE-KISKLSCEK-IL-18 (IL18) share high sequence
RT "cDNA cloning of biologically active chicken Interleukin-18.";
RL J. Interferon Cytokine Res. 20:879-883(2000).
DR EMBL; AJ27865; CAB96214.1; -.
DR InterPro; IPR008996; Cytok_IL1_like.
FT CHAIN 30 198 INTERLEUKIN 18.
FT CHAIN 30 198 INTERLEUKIN 18.
SQ SEQUENCE 198 AA; 22918 MW; 29BB77DC3E3C6600 CRC64;

Query Match 22.5%; Score 182.5; DB 13; Length 198;
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RESULT 14
Q9AV26 PRELIMINARY; PRT; 198 AA.
AC Q9AV26;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Interleukin-18 precursor (Fragment).
GN IL-18.
OS Meleagris gallopavo (Common turkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauromia; Aves; Neognathae; Galliformes; Phasianidae; Meleagris.
OX NCBI_TaxID=9103;
RN [1]
RP SEQUENCE FROM N.A.
RA Kaiser P.;
RT "Turkey and chicken interleukin-18 (IL18) share high sequence
RT identity, but have different polyadenylation sites in their 3' UTR.";
RL Dev. Comp. Immunol. 26:681-687(2002).
DR EMBL; AJ312000; CAC83483.1; -.
DR InterPro; IPR008996; Cytok_IL1_like.
KW Signal.
FT NON_TER 1
FT SIGNAL <1 28 POTENTIAL.
FT CHAIN 29 198 INTERLEUKIN-18.
SQ SEQUENCE 198 AA; 22967 MW; A1D450BC7207BFAD CRC64;

Query Match 22.7%; Score 184.5; DB 13; Length 198;
Best Local Similarity 34.9%; Pred. No. 2.2e-10;
Matches 58; Conservative 30; Mismatches 65; Indels 13; Gaps 7;

QY 2 FGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRNAPRTIFIISMVKDSQP-RG 59
DB 31 FCKETIKLFRNVNSQLLVVRPDLNMAAFEDVTDQEVKSGS-GMYFIHCYKTTAPSAG 89

QY 60 MAVTISVKCEKISKLSCEK-IL-18 (IL18) share high sequence
RT "cDNA cloning of biologically active chicken Interleukin-18.";
RL J. Interferon Cytokine Res. 20:879-883(2000).
DR EMBL; AJ27865; CAB96214.1; -.
DR InterPro; IPR008996; Cytok_IL1_like.
FT CHAIN 30 198 INTERLEUKIN 18.
FT CHAIN 30 198 INTERLEUKIN 18.
SQ SEQUENCE 198 AA; 22918 MW; 29BB77DC3E3C6600 CRC64;

Query Match 22.5%; Score 182.5; DB 13; Length 198;
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 19, 2004, 13:34:05 ; Search time 19 Seconds  
(without alignments)

426.594 Million cell updates/sec

Title: US-09-716-356A-6

Perfect score: 812

Sequence: 1 YFGKLESLKSLVIRNLNDQVL.....LKKEDELGRSMTFTVQVNE 157

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:\*

- 1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*
- 2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep:\*
- 3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:\*
- 4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*
- 5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\*
- 6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	811	99.9	157	4	US-08-982-285-4
2	811	99.9	157	4	US-09-700-609-1
3	811	99.9	158	4	US-09-398-412B-7
4	810	99.8	157	2	US-08-896-605A-6
5	810	99.8	157	2	US-08-896-501A-4
6	810	99.8	157	3	US-08-884-324-1
7	810	99.8	157	3	US-08-996-338-26
8	810	99.8	157	3	US-08-558-818-1
9	810	99.8	157	3	US-08-974-469A-1
10	810	99.8	157	3	US-08-832-180-1
11	810	99.8	157	3	US-08-832-198-6
12	810	99.8	157	4	US-09-819-902-6
13	810	99.8	157	4	US-09-752-510-6
14	810	99.8	157	4	US-09-711-899-1
15	810	99.8	157	4	US-09-556-972-26
16	810	99.8	157	4	US-09-649-063-1
17	810	99.8	193	2	US-08-896-605A-2
18	810	99.8	193	2	US-08-896-501A-2
19	810	99.8	193	3	US-08-832-180-9
20	801	98.6	157	4	US-08-982-285-6
21	792	97.5	193	4	US-09-597-576-2
22	791	97.4	157	4	US-08-982-285-7
23	791	97.4	157	4	US-08-982-285-8
24	782	96.3	157	4	US-08-982-285-11
25	781	96.2	157	4	US-08-982-285-9
26	772	95.1	157	4	US-08-982-285-12
27	771	95.0	157	4	US-08-982-285-10

28 613 75.5 179 4 US-09-445-724B-14 Sequence 14, Appl  
29 613 75.5 193 4 US-09-445-724B-2 Sequence 2, Appl  
30 613 75.5 193 4 US-09-445-724B-6 Sequence 6, Appl  
31 517 63.7 157 4 US-08-982-285-13 Sequence 13, Appl  
32 515 63.4 157 4 US-08-982-285-5 Sequence 5, Appl  
33 515 63.4 157 4 US-09-700-609-2 Sequence 2, Appl  
34 515 63.4 158 4 US-09-398-412B-8 Sequence 8, Appl  
35 513 63.2 157 2 US-08-502-535B-2 Sequence 2, Appl  
36 513 63.2 157 2 US-08-908-005A-2 Sequence 2, Appl  
37 513 63.2 157 3 US-08-996-338-27 Sequence 27, Appl  
38 513 63.2 157 3 US-08-558-818-7 Sequence 7, Appl  
39 513 63.2 157 3 US-08-974-469A-7 Sequence 7, Appl  
40 513 63.2 157 3 US-08-832-180-8 Sequence 8, Appl  
41 513 63.2 157 3 US-08-832-198-11 Sequence 11, Appl  
42 513 63.2 157 3 US-09-253-523-2 Sequence 2, Appl  
43 513 63.2 157 3 US-09-251-911-2 Sequence 2, Appl  
44 513 63.2 157 4 US-09-819-902-11 Sequence 11, Appl  
45 513 63.2 157 4 US-09-752-510-11 Sequence 11, Appl

#### ALIGNMENTS

RESULT 1  
US-08-982-285-4  
; Sequence 4, Application US/08982285  
; Patent No. 6476197  
; GENERAL INFORMATION:  
; APPLICANT: YAMAMOTO, Koza  
; APPLICANT: OKAMOTO, Iwao  
; APPLICANT: KURIMOTO, Masashi  
; TITLE OF INVENTION: POLYPEPTIDES  
; NUMBER OF SEQUENCES: 51  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.  
; STREET: 419 7th Street N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/982,285  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 333,037/96  
; FILING DATE: No. 6476197ember 29, 1996  
; APPLICATION NUMBER: JP 20,906/97  
; FILING DATE: January 21, 1997  
; APPLICATION NUMBER: JP 10,053,503  
; FILING DATE: No. 6476197ember 14, 1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROWDY, Roger L.  
; REGISTRATION NUMBER: 25,618  
; REFERENCE/DOCKET NUMBER: YAMAMOTO=15  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 157 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-982-285-4

Query Match 99.9%; Score 811; DB 4; Length 157;  
Best Local Similarity 99.4%; Pred. No. 3.8e-88;  
Matches 156; Conservative 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60  
 Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60  
 QY 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKDTKSDIIFQRSVPVGHDKMQFESSY 120  
 Db 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKDTKSDIIFQRSVPVGHDKMQFESSY 120  
 QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157  
 Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 2

US-09-700-609-1  
 ; Sequence 1, Application US/09700609  
 ; Patent No. 6582689  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Johnson, Randall K  
 ; FILE REFERENCE: P50777  
 ; CURRENT APPLICATION NUMBER: US/09/700,609  
 ; CURRENT FILING DATE: 2000-11-17  
 ; PRIOR APPLICATION NUMBER: 60/086,560  
 ; PRIOR FILING DATE: 1999-05-21  
 ; NUMBER OF SEQ ID NOS: 2  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 1  
 ; LENGTH: 157  
 ; TYPE: PRT  
 ; ORGANISM: Human  
 US-09-700-609-1

Query Match 99.9%; Score 811; DB 4; Length 157;  
 Best Local Similarity 99.4%; Pred. No. 3.8e-88;  
 Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60  
 Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60  
 QY 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKDTKSDIIFQRSVPVGHDKMQFESSY 120  
 Db 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKDTKSDIIFQRSVPVGHDKMQFESSY 120  
 QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157  
 Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 3

US-09-398-412B-7  
 ; Sequence 7, Application US/09398412B  
 ; Patent No. 6680380  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Timans, Jacqueline C.  
 ; TITLE OF INVENTION: Nucleic acids encoding mammalian interleukin-1zeta, related reage  
 ; FILE REFERENCE: DX0904K  
 ; CURRENT APPLICATION NUMBER: US/09/398,412B  
 ; CURRENT FILING DATE: 1999-09-17  
 ; PRIOR APPLICATION NUMBER: US 60/100948  
 ; PRIOR FILING DATE: 1998-09-18  
 ; NUMBER OF SEQ ID NOS: 15  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 7  
 ; LENGTH: 158  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-398-412B-7  
 Query Match 99.9%; Score 811; DB 4; Length 158;

Best Local Similarity 99.4%; Pred. No. 3.8e-88;  
 Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60  
 Db 2 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 61  
 QY 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKDTKSDIIFQRSVPVGHDKMQFESSY 120  
 Db 62 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKDTKSDIIFQRSVPVGHDKMQFESSY 121  
 QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157  
 Db 122 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 158

RESULT 4

US-08-896-605A-6  
 ; Sequence 6, Application US/08896605A  
 ; Patent No. 5879942  
 ; GENERAL INFORMATION:  
 ; APPLICANT: TANIMOTO, Tadao  
 ; APPLICANT: KURIMOTO, Masashi  
 ; TITLE OF INVENTION: PROCESSING ENZYME FOR POLYPEPTIDE  
 ; NUMBER OF SEQUENCES: 9  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: BROWDY AND NEIMARK  
 ; STREET: 419 Seventh Street, N.W., Suite 300  
 ; CITY: Washington  
 ; STATE: D.C.  
 ; COUNTRY: USA  
 ; ZIP: 20004  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SVSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/896,605A  
 ; FILING DATE: 18 July 1997  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: JP 207,691/1996  
 ; FILING DATE: 19-JUL-1996  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: JP 156,062/1997  
 ; FILING DATE: 30-MAY-1997  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: BROWDY, Roger L.  
 ; REGISTRATION NUMBER: 25,618  
 ; REFERENCE/DOCKET NUMBER: TANIMOTO-2  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 202-628-5197  
 ; TELEFAX: 202-737-3528  
 ; INFORMATION FOR SEQ ID NO: 6:  
 ; LENGTH: 157 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 US-08-896-605A-6

Query Match 99.8%; Score 810; DB 2; Length 157;  
 Best Local Similarity 100.0%; Pred. No. 4.9e-88;  
 Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60  
 Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60  
 QY 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKDTKSDIIFQRSVPVGHDKMQFESSY 120  
 Db 61 AVTISVKCEKISXLSKCNKIISFKEMNPPDNIKDTKSDIIFQRSVPVGHDKMQFESSY 120

QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157  
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

## RESULT 5

US-08-896-501A-4  
; Sequence 4, Application US/08896501A  
; Patent No. 5891663

GENERAL INFORMATION:  
; APPLICANT: TANIMOTO, Tadao  
; APPLICANT: KURIMOTO, Masashi  
; TITLE OF INVENTION: PROCESS FOR PRODUCING POLYPEPTIDE  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/896,501A  
; FILING DATE: 18-JUL-1997

PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 213,267/1996  
; FILING DATE: 25-JUL-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 31,474/1997  
; FILING DATE: 31-JAN-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROWDY, Roger L.  
; REGISTRATION NUMBER: 25,618  
; REFERENCE/DOCKET NUMBER: TANIMOTO=3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528

INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 157 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-896-501A-4

Query Match 99.8%; Score 810; DB 2; Length 157;  
Best Local Similarity 100.0%; Pred. No. 4.9e-88;  
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIIISMTYKDSQPRGM 60  
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIIISMTYKDSQPRGM 60  
QY 61 AVTISVKCEKISXLSCKENKIISFKEMNPPDNIKDTKSDIIFQRSVPVGHDKMQFESSY 120  
Db 61 AVTISVKCEKISXLSCKENKIISFKEMNPPDNIKDTKSDIIFQRSVPVGHDKMQFESSY 120  
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157  
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

## RESULT 6

US-08-884-324-1  
; Sequence 1, Application US/08884324  
; Patent No. 6060283

GENERAL INFORMATION:  
; APPLICANT: Takanori OKURA  
; APPLICANT: Kakuji TORIGOE  
; APPLICANT: Masahi KURIMOTO  
; TITLE OF INVENTION: GENOMIC DNA ENCODING A POLYPEPTIDE CAPABLE  
; TITLE OF INVENTION: OF INDUCING THE PRODUCTION OF INTERFERON-  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/884,324  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 185,305/96  
; FILING DATE: 27-JUN-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROWDY, Roger L.  
; REGISTRATION NUMBER: 25,618  
; REFERENCE/DOCKET NUMBER: OKURA=1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528

INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 157 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-884-324-1

Query Match 99.8%; Score 810; DB 3; Length 157;  
Best Local Similarity 100.0%; Pred. No. 4.9e-88;  
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIIISMTYKDSQPRGM 60  
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIIISMTYKDSQPRGM 60  
QY 61 AVTISVKCEKISXLSCKENKIISFKEMNPPDNIKDTKSDIIFQRSVPVGHDKMQFESSY 120  
Db 61 AVTISVKCEKISXLSCKENKIISFKEMNPPDNIKDTKSDIIFQRSVPVGHDKMQFESSY 120  
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157  
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

## RESULT 7

US-08-996-338-26  
; Sequence 26, Application US/08996338  
; Patent No. 6087116

GENERAL INFORMATION:  
; APPLICANT: TORIGOE, Kakuji  
; APPLICANT: OKURA, Takanori  
; APPLICANT: KURIMOTO, Masahi  
; TITLE OF INVENTION: POLYPEPTIDES  
; NUMBER OF SEQUENCES: 37  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.

```

; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/996,338
; FILING DATE: 22-DEC-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 74,697/1997
; FILING DATE: 12-MAR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 215,488/1997
; FILING DATE: 28-JUL-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 291,837/1997
; FILING DATE: 09-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: TORIGOE=3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-996-338-26

Query Match 99.8%; Score 810; DB 3; Length 157;
Best Local Similarity 100.0%; Pred. No. 4.9e-88;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRDNAPRTIFIISMVKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRDNAPRTIFIISMVKDSQPRGM 60
QY 61 AVTISVCKEKISXLSCEKNKIIISFKEMNPPDNIKDKTSDIIFQRSVPVGHDKNQFESSY 120
Db 61 AVTISVCKEKISXLSCEKNKIIISFKEMNPPDNIKDKTSDIIFQRSVPVGHDKNQFESSY 120
QY 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNEED 157
Db 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNEED 157

RESULT 8
US-08-558-818-1
; Sequence 1, Application US/08558818
; Patent No. 6197297
; GENERAL INFORMATION:
; APPLICANT: NAME: KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU
; APPLICANT: KENKYUJO
; APPLICANT: KUNIKATA, Toshio
; APPLICANT: TANIGUCHI, Mutsuko
; APPLICANT: KOHNO, Keizo
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFIC TO POLYPEPTIDE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street N.W. Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect Version 5.0
; ATTORNEY/AGENT INFORMATION:
; NAME: Browdy, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: FELICI=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/558,818
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: JP 58,240/95
; PRIOR APPLICATION DATA: February 23, 1995
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-558-818-1

Query Match 99.8%; Score 810; DB 3; Length 157;
Best Local Similarity 100.0%; Pred. No. 4.9e-88;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRDNAPRTIFIISMVKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCDRDNAPRTIFIISMVKDSQPRGM 60
QY 61 AVTISVCKEKISXLSCEKNKIIISFKEMNPPDNIKDKTSDIIFQRSVPVGHDKNQFESSY 120
Db 61 AVTISVCKEKISXLSCEKNKIIISFKEMNPPDNIKDKTSDIIFQRSVPVGHDKNQFESSY 120
QY 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNEED 157
Db 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNEED 157

RESULT 9
US-08-974-469A-1
; Sequence 1, Application US/08974469A
; Patent No. 6207641
; GENERAL INFORMATION:
; APPLICANT: KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU
; APPLICANT: KENKYUJO
; APPLICANT: TORIGOE, Kakuji
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: FUKUDA, Shigeharu
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: AGENT FOR SUSCEPTIVE DISEASE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street N.W. Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect Version 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,469A
; FILING DATE:
; CLASSIFICATION:
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/599,879
; FILING DATE:
; APPLICATION NUMBER: JP 78,357/95
; FILING DATE: March 10, 1995
; APPLICATION NUMBER: JP 274,988/95
; FILING DATE: September 29, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Browdy, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: TORIGOE-1A
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-974-469A-1

Query Match          99.8%; Score 810; DB 3; Length 157;
Best Local Similarity 100.0%; Pred. No. 4.9e-88;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTDSDCRDNAPRTIFIISMVKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTDSDCRDNAPRTIFIISMVKDSQPRGM 60
QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTSKDIIFQORSVPGHDNKKQFESSY 120
Db 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTSKDIIFQORSVPGHDNKKQFESSY 120
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157

RESULT 10
US-08-832-180-1
; Sequence 1, Application US/08832180
; Patent No. 6214584
; GENERAL INFORMATION:
; APPLICANT: KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU
; APPLICANT: KENKYUO
; APPLICANT: USHIO, Shimpei
; APPLICANT: TORIGOE, Kakuji
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: OKAMURA, Haruki
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: INTERFERON- PRODUCTION INDUCING
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Browdy and Neimark
; STREET: 419 Seventh Street N.W. Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect Version 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/832,180
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/721,018
; FILING DATE: 25-SEP-1996
; APPLICATION NUMBER: JP 95-270725
; FILING DATE: 26-SEP-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 96-067434

; APPLICATION NUMBER: JP 304,203/94
; FILING DATE: No. 6214584ember 15, 1994
; APPLICATION NUMBER: 10048102
; FILING DATE: September 18, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Browdy, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: USHIO-1
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-832-180-1

Query Match          99.8%; Score 810; DB 3; Length 157;
Best Local Similarity 100.0%; Pred. No. 4.9e-88;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTDSDCRDNAPRTIFIISMVKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTDSDCRDNAPRTIFIISMVKDSQPRGM 60
QY 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTSKDIIFQORSVPGHDNKKQFESSY 120
Db 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTSKDIIFQORSVPGHDNKKQFESSY 120
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157

RESULT 11
US-08-832-198-6
; Sequence 6, Application US/08832198
; Patent No. 6242255
; GENERAL INFORMATION:
; APPLICANT: AKITA, Kenji
; APPLICANT: NUKADA, Yoshiyuki
; APPLICANT: FUJII, Mitsukiyo
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PROTEIN WHICH INDUCES INTERLEUKIN-GAMMA
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSES: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/832,198
; FILING DATE: 08-APR-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/721,018
; FILING DATE: 25-SEP-1996
; APPLICATION NUMBER: JP 95-270725
; FILING DATE: 26-SEP-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 96-067434
```

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/
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: JP not yet received
/ FILING DATE: 29-FEB-1996
/ FILING DATE: 20-SEP-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: BROWDY, Roger L.
/ REGISTRATION NUMBER: 25,618
/ REFERENCE/DOCKET NUMBER: AKITA=1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202) 628-5197
/ TELEFAX: (202) 737-3528
/ INFORMATION FOR SEQ ID NO: 6:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 157 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ FEATURE:
/ OTHER INFORMATION: "Xaa" in position 73 is either
/ 'ile' or 'Thr'
/
US-08-832-198-6
Query Match 99.8%; Score 810; DB 3; Length 157;
Best Local Similarity 100.0%; Pred. No. 4.9e-88;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
QY 61 AVTISVKCEKISXLSKENKIISFKEMNPPDNIKDTSKDIIFQRSVPGHDNKKQPESSSY 120
Db 61 AVTISVKCEKISXLSKENKIISFKEMNPPDNIKDTSKDIIFQRSVPGHDNKKQPESSSY 120
QY 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNEED 157
Db 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNEED 157

RESULT 12
US-09-819-902-6
/ Sequence 6, Application US/09819902
/ Patent No. 6403079
/ GENERAL INFORMATION:
/ APPLICANT: AKITA, Kenji
/ NUKADA, Yoshiyuki
/ FUJII, Mitsukiyo
/ TANIMOTO, Tadao
/ KURIMOTO, Masashi
/
/ TITLE OF INVENTION: PROTEIN WHICH INDUCES INTERLEUKIN-GAMMA
/
/ NUMBER OF SEQUENCES: 11
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
/ STREET: 419 Seventh Street N.W., Ste. 300
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: USA
/ ZIP: 20004
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/819,902
/ FILING DATE: 29-Mar-2001
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/832,798
/ FILING DATE: 25-SEP-1996
/ APPLICATION NUMBER: JP 95-270725
/
```

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/
/ FILING DATE: 26-SEP-1995
/ APPLICATION NUMBER: JP 96-067434
/ FILING DATE: 29-FEB-1996
/ APPLICATION NUMBER: JP not yet received
/ FILING DATE: 20-SEP-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: BROWDY, Roger L.
/ REGISTRATION NUMBER: 25,618
/ REFERENCE/DOCKET NUMBER: AKITA=1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202) 628-5197
/ TELEFAX: (202) 737-3528
/ INFORMATION FOR SEQ ID NO: 6:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 157 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ FEATURE:
/ OTHER INFORMATION: "Xaa" in position 73 is either
/ 'ile' or 'Thr'
/
US-09-819-902-6
Query Match 99.8%; Score 810; DB 4; Length 157;
Best Local Similarity 100.0%; Pred. No. 4.9e-88;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60
QY 61 AVTISVKCEKISXLSKENKIISFKEMNPPDNIKDTSKDIIFQRSVPGHDNKKQPESSSY 120
Db 61 AVTISVKCEKISXLSKENKIISFKEMNPPDNIKDTSKDIIFQRSVPGHDNKKQPESSSY 120
QY 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNEED 157
Db 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNEED 157

RESULT 13
US-09-752-510-6
/ Sequence 6, Application US/09752510
/ Patent No. 6441138
/ GENERAL INFORMATION:
/ APPLICANT: AKITA, Kenji
/ NUKADA, Yoshiyuki
/ FUJII, Mitsukiyo
/ TANIMOTO, Tadao
/ KURIMOTO, Masashi
/
/ TITLE OF INVENTION: PROTEIN WHICH INDUCES INTERLEUKIN-GAMMA
/
/ NUMBER OF SEQUENCES: 11
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
/ STREET: 419 Seventh Street N.W., Ste. 300
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: USA
/ ZIP: 20004
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/752,510
/ FILING DATE: 03-Jan-2001
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/721,018
/ FILING DATE: <Unknown>
/
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APPLICATION NUMBER: JP 96-067434  
FILING DATE: 29-FEB-1996  
APPLICATION NUMBER: JP not yet received  
FILING DATE: 20-SEP-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: AKITA=1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 628-5197  
TELEFAX: (202) 737-3528  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 157 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
OTHER INFORMATION: "Xaa" in position 73 is either  
'ile' or 'Thr'  
SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-09-752-510-6

Query Match 99.8%; Score 810; DB 4; Length 157;  
Best Local Similarity 100.0%; Pred. No. 4.9e-88;  
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCDRDNAPRTFIISMYKDSQPRGM 60  
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCDRDNAPRTFIISMYKDSQPRGM 60  
QY 61 AVTISVKCEKISXLSCEKNKIISFKEMNPPDNIKDTSDIIFQRSVPGHDKMQFESSY 120  
DB 61 AVTISVKCEKISXLSCEKNKIISFKEMNPPDNIKDTSDIIFQRSVPGHDKMQFESSY 120  
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157  
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157

RESULT 14  
US-09-711-899-1  
Sequence 1, Application US/09711899  
Patent No. 6509449  
GENERAL INFORMATION:  
APPLICANT: <Unknown>  
TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFIC TO POLYPEPTIDE  
WHICH INDUCES INTERFERON- PRODUCTION  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Browdy and Neimark  
STREET: 419 Seventh Street N.W. Ste. 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect Version 5.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/711,899  
FILING DATE: 13-NOV-6509449-2000  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/588,818  
FILING DATE: 2000-11-15  
ATTORNEY/AGENT INFORMATION:  
NAME: Browdy, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: FELICI=1

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 628-5197  
TELEFAX: (202) 737-3528  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 157 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-711-899-1

Query Match 99.8%; Score 810; DB 4; Length 157;  
Best Local Similarity 100.0%; Pred. No. 4.9e-88;  
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCDRDNAPRTFIISMYKDSQPRGM 60  
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCDRDNAPRTFIISMYKDSQPRGM 60  
QY 61 AVTISVKCEKISXLSCEKNKIISFKEMNPPDNIKDTSDIIFQRSVPGHDKMQFESSY 120  
DB 61 AVTISVKCEKISXLSCEKNKIISFKEMNPPDNIKDTSDIIFQRSVPGHDKMQFESSY 120  
QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157  
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157

RESULT 15  
US-09-556-972-26  
Sequence 26, Application US/09556972  
Patent No. 6559298  
GENERAL INFORMATION:  
APPLICANT: TORIGOE, Kakuji  
OKURA, Takanori  
KURIMOTO, Masashi  
TITLE OF INVENTION: POLYPEPTIDES  
NUMBER OF SEQUENCES: 37  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/556,972  
FILING DATE: 24-Apr-2000  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/996,338  
FILING DATE: 22-DEC-1997  
APPLICATION NUMBER: JP 74,697/1997  
FILING DATE: 12-MAR-1997  
APPLICATION NUMBER: JP 215,488/1997  
FILING DATE: 28-JUL-1997  
APPLICATION NUMBER: JP 291,837/1997  
FILING DATE: 09-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER: TORIGOE=3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 157

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;
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-556-972-26

Query Match      99.8%; Score 810; DB 4; Length 157;
Best Local Similarity 100.0%; Pred. No. 4.9e-88;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPFLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTKSDIIFQRSVPGHDNKKMQFESSY 120
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 61 AVTISVKCEKISXLSCEKNIISFKEMNPPDNIKDTKSDIIFQRSVPGHDNKKMQFESSY 120
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157
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Search completed: August 19, 2004, 13:37:15
Job time : 20 secs

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Result	Query	Score	Length	ID	Description
No.	Match				

1	811	99.9	157	9	US-09-775-046-9	Sequence 9, Appli
2	811	99.9	157	10	US-09-030-061-6	Sequence 6, Appli
3	811	99.9	157	12	US-10-247-703-65	Sequence 65, Appli
4	811	99.9	157	12	US-10-247-703-71	Sequence 71, Appli
5	811	99.9	157	13	US-10-100-057-6	Sequence 6, Appli
6	811	99.9	157	13	US-10-094-153-2	Sequence 2, Appli
7	811	99.9	157	14	US-10-260-576-4	Sequence 4, Appli
8	811	99.9	157	14	US-10-297-136-1	Sequence 1, Appli
9	811	99.9	157	15	US-10-311-491-3	Sequence 3, Appli
10	811	99.9	157	15	US-10-397-786A-3	Sequence 3, Appli
11	811	99.9	157	16	US-10-280-609-1	Sequence 1, Appli
12	811	99.9	157	16	US-10-646-308-14	Sequence 14, Appli
13	811	99.9	158	12	US-10-695-195-7	Sequence 7, Appli
14	811	99.9	158	16	US-10-694-978-7	Sequence 7, Appli
15	811	99.9	177	12	US-10-247-703-69	Sequence 69, Appli

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US-09-775-046-9
; Sequence 9, Application US/09775046
; Patent No. US20020102234A1
; GENERAL INFORMATION:
; APPLICANT: Debets, Johannes Eduard
; APPLICANT: Timans, Jacqueline C.
; APPLICANT: Bazan, J. Fernando
; APPLICANT: Kastelein, Robert A.
; TITLE OF INVENTION: MAMMALIAN CYTO
; FILE REFERENCE: DX01073K
; CURRENT APPLICATION NUMBER: US/09/
; CURRENT FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: 60/179,6
; PRIOR FILING DATE: 2000-02-02
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 157
; TYPE: prt
; ORGANISM: Homo sapiens
US-09-775-046-9

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	Query Match	99.9%	Score 811;	DB 9;	Length 157;
	Best Local Similarity	99.4%;	Pred. No. 3.1e-81;		
	Matches 156;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
Qy	1	YFGKLESKSVIRNLNDQVLFIDQGNRPLEDMTDSDCRDNPRTFIISWYKDSQPRGM	60		
Db	1	YFGKLESKSVIRNLNDQVLFIDQGNRPLEDMTDSDCRDNPRTFIISWYKDSQPRGM	60		
Qy	61	AVTISVKCEKISXLSNCENKIISPKEMPPPNIIKDTKSDIIFFORSVPGHNKMQFESSY	120		
Db	61	AVTISVKCEKISXLSNCENKIISPKEMPPPNIIKDTKSDIIFFORSVPGHNKMQFESSY	120		
Qy	121	EGYFLACEKRDRLFKLILKXKDELDGDRSIMFTVQNE	157		
Db	121	EGYFLACEKRDRLFKLILKXKDELDGDRSIMFTVQNE	157		

## RESULT 2

US-09-030-061-6  
; Sequence 6, Application US/09030061  
; Publication No. US20030095946A1  
; GENERAL INFORMATION:  
; APPLICANT: GILLISPIE, Matthew Todd  
; APPLICANT: HORWOOD, Nicole Joy  
; APPLICANT: UDAGAWA, NO. US20030095946Aluyuki  
; APPLICANT: KURIMOTO, Masashi  
; TITLE OF INVENTION: OSTEOCLASTGENIC INHIBITORY AGENT  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/030,061  
; FILING DATE: 25-FEB-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 55,468/1997  
; FILING DATE: 25-FEB-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROWDY, Roger L.  
; REGISTRATION NUMBER: 25,618  
; REFERENCE/DOCKET NUMBER: GILLISPIE-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 628-5197  
; TELEFAX: (202) 737-3528  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 157 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-09-030-061-6

Query Match 99.9%; Score 811; DB 10; Length 157;  
Best Local Similarity 99.4%; Pred. No. 3.1e-81;  
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60  
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60  
  
Qy 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIKOTKSDIIFQRSVPGHDNKKMQPESSSY 120  
Db 61 AVTISVKCEKISTLSCENKIISFKEMNPPDNIKOTKSDIIFQRSVPGHDNKKMQPESSSY 120  
  
Qy 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNEED 157  
Db 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNEED 157

## RESULT 3

US-10-247-703-65  
; Sequence 65, Application US/10247703  
; Publication No. US20030063597A1  
; GENERAL INFORMATION:  
; APPLICANT: Branigan, Patrick  
; APPLICANT: Goletz, Theresa J  
; APPLICANT: Knight, David M  
; APPLICANT: McCarthy, Stephen G  
; APPLICANT: Scallion, Bernard J

; APPLICANT: Snyder, Linda A  
; TITLE OF INVENTION: NUCLEIC ACID VACCINES USING TUMOR ANTIGEN ENCODING NUCLEIC ACIDS  
; FILE REFERENCE: CEN310  
; CURRENT APPLICATION NUMBER: US/10/247,703  
; CURRENT FILING DATE: 2002-09-20  
; PRIOR APPLICATION NUMBER: 60/328,371  
; PRIOR FILING DATE: 2001-10-10  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 65  
; LENGTH: 157  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-247-703-65

Query Match 99.9%; Score 811; DB 12; Length 157;  
Best Local Similarity 99.4%; Pred. No. 3.1e-81;  
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60  
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60  
  
Qy 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIKOTKSDIIFQRSVPGHDNKKMQPESSSY 120  
Db 61 AVTISVKCEKISTLSCENKIISFKEMNPPDNIKOTKSDIIFQRSVPGHDNKKMQPESSSY 120  
  
Qy 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNEED 157  
Db 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNEED 157

## RESULT 4

US-10-247-703-71  
; Sequence 71, Application US/10247703  
; Publication No. US20030063597A1  
; GENERAL INFORMATION:  
; APPLICANT: Branigan, Patrick  
; APPLICANT: Goletz, Theresa J  
; APPLICANT: Knight, David M  
; APPLICANT: McCarthy, Stephen G  
; APPLICANT: Scallion, Bernard J  
; APPLICANT: Snyder, Linda A  
; TITLE OF INVENTION: NUCLEIC ACID VACCINES USING TUMOR ANTIGEN ENCODING NUCLEIC ACIDS  
; FILE REFERENCE: CEN310  
; CURRENT APPLICATION NUMBER: US/10/247,703  
; CURRENT FILING DATE: 2002-09-20  
; PRIOR APPLICATION NUMBER: 60/328,371  
; PRIOR FILING DATE: 2001-10-10  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 71  
; LENGTH: 157  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-247-703-71

Query Match 99.9%; Score 811; DB 12; Length 157;  
Best Local Similarity 99.4%; Pred. No. 3.1e-81;  
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60  
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMYKDSQPRGM 60  
  
Qy 61 AVTISVKCEKISLSCENKIISFKEMNPPDNIKOTKSDIIFQRSVPGHDNKKMQPESSSY 120  
Db 61 AVTISVKCEKISTLSCENKIISFKEMNPPDNIKOTKSDIIFQRSVPGHDNKKMQPESSSY 120  
  
Qy 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNEED 157  
Db 121 EGYFLACEKERDLFKLLKKEDELGDRSIMFTVQNEED 157

Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 5  
US-10-100-057-6  
; Sequence 6, Application US/101000057  
; Publication No. US20020150555A1  
; GENERAL INFORMATION:  
; APPLICANT: GILLISPIE, Matthew Todd  
; HORWOOD, Nicole Joy  
; UDAGAWA, No. US20020150555A1uyuki  
; KURIMOTO, Masashi  
; TITLE OF INVENTION: OSTEOCLASTGENIC INHIBITORY AGENT  
; NUMBER OF SEQUENCES: 28  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA: US/10/100,057  
; FILING DATE: 19-Mar-2002  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/030,061  
; FILING DATE: 25-FEB-1998  
; APPLICATION NUMBER: JP 55,468/1997  
; FILING DATE: 25-FEB-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROWDY, Roger L.  
; REGISTRATION NUMBER: 25,618  
; REFERENCE/DOCKET NUMBER: GILLISPIE-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 628-5197  
; TELEFAX: (202) 737-3528  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 157 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-10-100-057-6

Query Match 99.9%; Score 811; DB 13; Length 157;  
Best Local Similarity 99.4%; Pred. No. 3.1e-81;  
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60  
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60

Qy 61 AVTISVKCEKISLSCENKIISFKEMNPPDNKDTKSDIIFQRSVPGHDKMKQFESSY 120  
Db 61 AVTISVKCEKISLSCENKIISFKEMNPPDNKDTKSDIIFQRSVPGHDKMKQFESSY 120

Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157  
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 6  
US-10-094-153-2  
; Sequence 2, Application US/10094153  
; Publication No. US20020169291A1  
; GENERAL INFORMATION:  
; APPLICANT: Dinarello, Charles

; APPLICANT: Kim, Soo Hyun  
; TITLE OF INVENTION: Interleukin-18 Mutants, Their Production and use  
; FILE REFERENCE: 475  
; CURRENT APPLICATION NUMBER: US/10/094,153  
; CURRENT FILING DATE: 2002-03-08  
; PRIOR APPLICATION NUMBER: 60/274,327  
; PRIOR FILING DATE: 2001-03-08  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: Patent In version 3.1  
; SEQ ID NO 2  
; LENGTH: 157  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-094-153-2

Query Match 99.9%; Score 811; DB 13; Length 157;  
Best Local Similarity 99.4%; Pred. No. 3.1e-81;  
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60  
Db 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60

Qy 61 AVTISVKCEKISLSCENKIISFKEMNPPDNKDTKSDIIFQRSVPGHDKMKQFESSY 120  
Db 61 AVTISVKCEKISLSCENKIISFKEMNPPDNKDTKSDIIFQRSVPGHDKMKQFESSY 120

Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157  
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 7  
US-10-260-576-4  
; Sequence 4, Application US/10260576  
; Publication No. US20030092130A1  
; GENERAL INFORMATION:  
; APPLICANT: YAMAMOTO, Koza  
; KURIMOTO, Masashi  
; TITLE OF INVENTION: POLYPEPTIDES  
; NUMBER OF SEQUENCES: 51  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.  
; STREET: 419 7th Street N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA: US/10/260,576  
; FILING DATE: 01-Oct-2002  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/982,285  
; FILING DATE: <Unknown>  
; APPLICATION NUMBER: JP 333,037/96  
; FILING DATE: NO. US20030092130A1ember 29, 1996  
; APPLICATION NUMBER: JP 20,906/97  
; FILING DATE: January 21, 1997  
; APPLICATION NUMBER: JP 10,053,503  
; FILING DATE: NO. US20030092130A1ember 14, 1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROWDY, Roger L.  
; REGISTRATION NUMBER: 25,618  
; REFERENCE/DOCKET NUMBER: YAMAMOTO=15  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528

```
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 157 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-260-576-4

Query Match          99.9%; Score 811; DB 14; Length 157;
Best Local Similarity 99.4%; Pred. No. 3.1e-81;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMVKDSQPRGM 60
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMVKDSQPRGM 60

QY 61 AVTISVKCEKISXLSCEKNKIIISFKEMNPPDNIKDTKSDIIFQRSVPVGHDKMKQFESSY 120
DB 61 AVTISVKCEKISXLSCEKNKIIISFKEMNPPDNIKDTKSDIIFQRSVPVGHDKMKQFESSY 120

QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 8
US-10-297-136-1
; Sequence 1, Application US/10297136
; Publication No. US20030113292A1
; GENERAL INFORMATION:
; APPLICANT: ESSER, KLAUS M.
; APPLICANT: ROSENBERG, MARTIN
; APPLICANT: TAL-SINGER, RUTH
; APPLICANT: WOODNUTT, GARY
; APPLICANT: CHISARI, FRANCIS V.
; APPLICANT: DILLON, SUSAN B.
; TITLE OF INVENTION: Methods of Treating Viral Diseases with
; FILE REFERENCE: P51144
; CURRENT APPLICATION NUMBER: US/10/297,136
; PRIOR FILING DATE: 2002-10-02
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: 60/208,869
; PRIOR FILING DATE: 2000-06-02
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-297-136-1

Query Match          99.9%; Score 811; DB 14; Length 157;
Best Local Similarity 99.4%; Pred. No. 3.1e-81;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMVKDSQPRGM 60
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMVKDSQPRGM 60

QY 61 AVTISVKCEKISXLSCEKNKIIISFKEMNPPDNIKDTKSDIIFQRSVPVGHDKMKQFESSY 120
DB 61 AVTISVKCEKISXLSCEKNKIIISFKEMNPPDNIKDTKSDIIFQRSVPVGHDKMKQFESSY 120

QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 9
US-10-311-491-3
; Sequence 3, Application US/10311491
; Publication No. US20030143198A1
; GENERAL INFORMATION:
; APPLICANT: Johanson, Kyung O.
; APPLICANT: Kirkpatrick, Robert B.
; APPLICANT: Shatzman, Allan R.
; APPLICANT: Ho, Yen Sen
; APPLICANT: McDevitt, Damien
; TITLE OF INVENTION: Method for Preparing a Physiologically
; FILE REFERENCE: P51137
; CURRENT APPLICATION NUMBER: US/10/311,491
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/US01/18804
; PRIOR FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: 60/211,832
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/224,128
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: 60/264,923
; PRIOR FILING DATE: 2001-01-20
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-311-491-3

Query Match          99.9%; Score 811; DB 14; Length 157;
Best Local Similarity 99.4%; Pred. No. 3.1e-81;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMVKDSQPRGM 60
DB 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMVKDSQPRGM 60

QY 61 AVTISVKCEKISXLSCEKNKIIISFKEMNPPDNIKDTKSDIIFQRSVPVGHDKMKQFESSY 120
DB 61 AVTISVKCEKISXLSCEKNKIIISFKEMNPPDNIKDTKSDIIFQRSVPVGHDKMKQFESSY 120

QY 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157
DB 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157

RESULT 10
US-10-397-786A-3
; Sequence 3, Application US/10397786A
; Publication No. US20040018195A1
; GENERAL INFORMATION:
; APPLICANT: Griswold, Donald
; APPLICANT: Li, Li
; APPLICANT: Li, Jian
; TITLE OF INVENTION: DIABETES DISEASE DERIVED PROTEINS, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN-0287
; CURRENT APPLICATION NUMBER: US/10/397,786A
; CURRENT FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: 60/367,902
; PRIOR FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver 2.0
; SEQ ID NO 3
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-397-786A-3

Query Match          99.9%; Score 811; DB 15; Length 157;
Best Local Similarity 99.4%; Pred. No. 3.1e-81;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMVKDSQPRGM 60
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Db 1 YFGKLESKLSVIRNLDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60  
61 AVTISVKCEKISXLSCEKNKISFKEMNPPDNKDKTSDIIFQSVPGHDNKKMQFESSY 120  
Db 61 AVTISVKCEKISXLSCEKNKISFKEMNPPDNKDKTSDIIFQSVPGHDNKKMQFESSY 120  
Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157  
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157

RESULT 11

US-10-280-609-1  
; Sequence 1, Application US/10280609  
; Publication No. US2004002336A1  
; GENERAL INFORMATION:  
; APPLICANT: Heavner, George  
; APPLICANT: Snyder, Linda Anne  
; APPLICANT: McCarthy, Stephen G.  
; TITLE OF INVENTION: IL-18 OR MUT-IL-18R PROTEINS, ANTIBODIES, COMPOSITIONS,  
; TITLE OF INVENTION: METHODS AND USES  
; FILE REFERENCE: CEN0321  
; CURRENT APPLICATION NUMBER: US/10/280,609  
; CURRENT FILING DATE: 2002-10-25  
; PRIOR APPLICATION NUMBER: 60/335,880  
; PRIOR FILING DATE: 2001-10-26  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: PatentIn Ver 3.1  
; SEQ ID NO 1  
; LENGTH: 157  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-280-609-1

Query Match 99.9%; Score 811; DB 16; Length 157;  
Best Local Similarity 99.4%; Pred. No. 3.1e-81;  
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 YFGKLESKLSVIRNLDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60  
Db 1 YFGKLESKLSVIRNLDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60  
Qy 61 AVTISVKCEKISXLSCEKNKISFKEMNPPDNKDKTSDIIFQSVPGHDNKKMQFESSY 120  
Db 61 AVTISVKCEKISXLSCEKNKISFKEMNPPDNKDKTSDIIFQSVPGHDNKKMQFESSY 120  
Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157  
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157

RESULT 12

US-10-646-308-14  
; Sequence 14, Application US/10646308  
; Publication No. US20040136992A1  
; GENERAL INFORMATION:  
; APPLICANT: BURTON, Paul B. J.  
; APPLICANT: DEISHER, Theresa A.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING CARDIOVASCULAR DISEASE  
; FILE REFERENCE: 3432-B  
; CURRENT APPLICATION NUMBER: US/10/646,308  
; CURRENT FILING DATE: 2003-08-21  
; PRIOR APPLICATION NUMBER: --to be assigned--  
; PRIOR FILING DATE: 2003-08-12  
; PRIOR APPLICATION NUMBER: 60/406,418  
; PRIOR FILING DATE: 2002-08-28  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 14  
; LENGTH: 157  
; TYPE: PRT  
; ORGANISM: Homo sapiens

US-10-646-308-14

Query Match 99.9%; Score 811; DB 16; Length 157;  
Best Local Similarity 99.4%; Pred. No. 3.1e-81;  
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 YFGKLESKLSVIRNLDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60  
Db 1 YFGKLESKLSVIRNLDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60  
Qy 61 AVTISVKCEKISXLSCEKNKISFKEMNPPDNKDKTSDIIFQSVPGHDNKKMQFESSY 120  
Db 61 AVTISVKCEKISXLSCEKNKISFKEMNPPDNKDKTSDIIFQSVPGHDNKKMQFESSY 120  
Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157  
Db 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNEED 157

RESULT 13

US-10-695-195-7  
; Sequence 7, Application US/10695195  
; Publication No. US20040068099A1  
; GENERAL INFORMATION:  
; APPLICANT: Timans, Jacqueline C.  
; TITLE OF INVENTION: Mammalian Cytokines; Related Reagents and Methods  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/695,195  
; FILING DATE: 27-Oct-2003  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/398,412  
; FILING DATE: 17-Sep-1999  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0904K  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650)852-9196  
; TELEFAX: (650)496-1200  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 158 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
US-10-695-195-7

Query Match 99.9%; Score 811; DB 12; Length 158;  
Best Local Similarity 99.4%; Pred. No. 3.1e-81;  
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 YFGKLESKLSVIRNLDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 60  
Db 2 YFGKLESKLSVIRNLDQVLFIDQGNRPLFEDMTSDCRDNAPRTIFIISMVKDSQPRGM 61  
Qy 61 AVTISVKCEKISXLSCEKNKISFKEMNPPDNKDKTSDIIFQSVPGHDNKKMQFESSY 120

Db 62 AVTISVKCEKISTLSCENKIIISFKEMNPPDNIKOTKSDIIFFQRSVPGHDNKMQPESSSY 121  
Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157  
Db 122 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 158

## RESULT 14

US-10-694-978-7  
; Sequence 7, Application US/10694978  
; Publication No. US20040087766A1  
; GENERAL INFORMATION:  
; APPLICANT: Timans, Jacqueline C.  
; TITLE OF INVENTION: Mammalian Cytokines; Related Reagents and Methods  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: DNAX Research Institute  
; STREET: 901 California Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; FILING DATE: 27-Oct-2003  
; APPLICATION NUMBER: US/10/694,978  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/398,412  
; FILING DATE: 17-Sep-1999  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34,090  
; REFERENCE/DOCKET NUMBER: DX0904K  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650)852-9196  
; TELEFAX: (650)496-1200  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
US-10-694-978-7

Query Match 99.9%; Score 811; DB 16; Length 158;  
Best Local Similarity 99.4%; Pred. No. 3.1e-81;  
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60  
Db 2 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 61  
Qy 61 AVTISVKCEKISXLSCEKIIISFKEMNPPDNIKOTKSDIIFFQRSVPGHDNKMQPESSSY 120  
Db 62 AVTISVKCEKISTLSCENKIIISFKEMNPPDNIKOTKSDIIFFQRSVPGHDNKMQPESSSY 121  
Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157  
Db 122 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 158

## RESULT 15

US-10-247-703-69  
; Sequence 69, Application US/10247703  
; Publication No. US20030063597A1  
; GENERAL INFORMATION:

; APPLICANT: Branigan, Patrick  
; APPLICANT: Goletz, Theresa J  
; APPLICANT: Knight, David M  
; APPLICANT: McCarthy, Stephen G  
; APPLICANT: Scallion, Bernard J  
; APPLICANT: Snyder, Linda A  
; TITLE OF INVENTION: NUCLEIC ACID VACCINES USING TUMOR ANTIGEN ENCODING NUCLEIC ACIDS  
; TITLE OF INVENTION: CYTOKINE ADJUVANT ENCODING NUCLEIC ACID  
; FILE REFERENCE: CEN310  
; CURRENT APPLICATION NUMBER: US/10/247,703  
; CURRENT FILING DATE: 2002-09-20  
; PRIOR APPLICATION NUMBER: 60/328,371  
; PRIOR FILING DATE: 2001-10-10  
; NUMBER OF SEQ ID NOS: 77  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 69  
; LENGTH: 177  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-247-703-69

Query Match 99.9%; Score 811; DB 12; Length 177;  
Best Local Similarity 99.4%; Pred. No. 3.6e-81;  
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 60  
Db 21 YFGKLESKLSVIRNLNDQVLFIDQGNRPLFEDMTDSDCRDNAPRTIFIISMYKDSQPRGM 80  
Qy 61 AVTISVKCEKISXLSCEKIIISFKEMNPPDNIKOTKSDIIFFQRSVPGHDNKMQPESSSY 120  
Db 81 AVTISVKCEKISTLSCENKIIISFKEMNPPDNIKOTKSDIIFFQRSVPGHDNKMQPESSSY 140  
Qy 121 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 157  
Db 141 EGYFLACEKERDLFKLILKKEDELGDRSIMFTVQNE 177

Search completed: August 19, 2004, 13:38:12  
Job time : 46 secs